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ATTORNEY'S DOCKET NUMBER  
S-137-1103/SG/A/SGS/PCT

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

09/180798

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. 371**

INTERNATIONAL APPLICATION NO. PCT/ EP 97/02443	INTERNATIONAL FILING DATE 13 May 1997 (13.05.97)	PRIORITY DATE CLAIMED 14 May 1996 (14.05.96)
TITLE OF INVENTION PRODUCTION OF APOMIETIC SEED		
APPLICANT(S) FOR DO/EO/US DE VRIES ET AL.		

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1.  This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2.  This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3.  This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4.  A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5.  A copy of the International Application as filed (35 U.S.C. 371(c)(2))
  - a.  is transmitted herewith (required only if not transmitted by the International Bureau).
  - b.  has been transmitted by the International Bureau. (See Form PCT/IB/308)
  - c.  is not required, as the application was filed in the United States Receiving Office (RO/US).
6.  A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7.  Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
  - a.  are transmitted herewith (required only if not transmitted by the International Bureau).
  - b.  have been transmitted by the International Bureau.
  - c.  have not been made; however, the time limit for making such amendments has NOT expired.
  - d.  have not been made and will not be made.
8.  A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9.  An executed Declaration and Power of Attorney (original or copy) (35 U.S.C. 371(c)(4)).
10.  A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

**Items 11. to 16. below concern document(s) or information included.**

11.  An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12.  An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13.  A **FIRST** preliminary amendment.  
 A **SECOND** or **SUBSEQUENT** preliminary amendment.
14.  A substitute specification.
15.  A change of power of attorney and/or address letter.
16.  Other items or information:

U.S. APPLICATION NO (if known, see 37 CFR 1.5)	INTERNATIONAL APPLICATION NO PCT/ EP 97/02443	ATTORNEY'S DOCKET NUMBER S-137-1103/SG/A/SGS/PCT
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17.  The following fees are submitted:

**BASIC NATIONAL FEE (37 CFR 1.492(a) (1)-(5)):**

		CALCULATIONS PTO USE ONLY
Search Report has been prepared by the EPO or JPO .....	\$930	
International preliminary examination fee paid to USPTO (37 CFR 1.482) .....	\$720	
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) .....	\$790	
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO.....	\$1,070	
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4). ....	\$98	

**ENTER APPROPRIATE BASIC FEE AMOUNT =**

\$ 930

Surcharge of \$130 for furnishing the oath of declaration later than  20  30 months from the earliest claimed priority date (37 CFR 1.492(e)).

\$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	
Total claims	46	- 20 =	26	X \$ 22 \$ 572
Independent claims	5	- 3 =	2	X \$ 82 \$ 164
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 270	\$

**TOTAL OF ABOVE CALCULATIONS =** \$ 1666

Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28).

**SUBTOTAL =** \$ 1666

Processing fee of \$130 for furnishing the English translation later than  20  30 months from the earliest claimed priority date (37 CFR 1.492(f)).

\$

**TOTAL NATIONAL FEE =** \$ 1666

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40 per property

\$

**TOTAL FEES ENCLOSED =** \$ 1666

Amount to be:	\$
refunded	
charged	\$

- a.  A check in the amount of \$ \_\_\_\_\_ to cover the above fees is enclosed.
- b.  Please charge Deposit Account No. 19-0134 in the amount of \$1666 to cover the above fees. A duplicate copy of this form is enclosed.
- c.  The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 19-0134.

**NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.**

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Production of Apomictic Seed

The present invention relates to the production of genetically transformed plants. In particular the invention relates *inter alia* to a process for inducing apomixis, to the apomictic seeds which result from the process, and to the plants and progeny thereof which result from the germination of such seeds.

Apomixis, which is vegetative (non-sexual) reproduction through seeds, is a genetically controlled reproductive mechanism found in some polyploid non-cultivated species. The process is classified as gametophytic or non-gametophytic. In gametophytic apomixis - of which there are two types (apospory and diplospory), multiple embryo sacs which typically lack antipodal nuclei are formed, or else megasporogenesis in the embryo sac takes place. In adventitious embryony (non-gametophytic apomixis), a somatic embryo develops directly from the cells of the embryo sac, ovary wall or integuments. In adventitious embryony, somatic embryos from surrounding cells invade the sexual ovary, one of the somatic embryos out-competes the other somatic embryos and the sexual embryo and utilizes the produced endosperm.

Were apomixis to be a controllable and reproducible phenomenon it would provide many advantages in plant improvement and cultivar development in the case that sexual plants are available as crosses with the apomictic plant.

For example, apomixis would provide for true-breeding, seed propagated hybrids. Moreover, apomixis could shorten and simplify the breeding process so that selfing and progeny testing to produce and/or stabilize a desirable gene combination could be eliminated. Apomixis would provide for the use as cultivars of genotypes with unique gene combinations since apomictic genotypes breed true irrespective of heterozygosity. Genes or groups of genes could thus be "pyramided and "fixed" in super genotypes. Every superior apomictic genotype from a sexual-apomictic cross would have the potential to be a cultivar. Apomixis would allow plant breeders to develop cultivars with specific stable traits for such characters as height, seed and forage quality and maturity. Breeders would not be limited in their commercial production of hybrids by (i) a cytoplasmic-nuclear interaction to produce male sterile female parents or (ii) the fertility restoring

capacity of a pollinator. Almost all cross-compatible germplasm could be a potential parent to produce apomictic hybrids.

Finally, apomixis would simplify commercial hybrid seed production. In particular, (i) the need for physical isolation of commercial hybrid production fields would be eliminated; (ii) all available land could be used to increase hybrid seed instead of dividing space between pollinators and male sterile lines; and (iii) the need to maintain parental line seed stocks would be eliminated.

The potential benefits to accrue from the production of seed via apomixis are presently unrealized, to a large extent because of the problem of engineering apomictic capacity into plants of interest. The present invention provides a solution to that problem in that it provides the means for obtaining plants which exhibit the adventitious embryony type of apomixis.

According to the present invention there is provided a method of producing apomictic seeds comprising the steps of:

- (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic,
- (ii) regenerating the thus transformed material into plants, or carpel-containing parts thereof, and
- (iii) expressing the sequence in the vicinity of the embryo sac.

By "vicinity of the embryo sac" is meant in one or more of the following: carpel, integuments, ovule, ovule premordium, ovary wall, chalaza, nucellus, funicle and placenta. The skilled man will recognize that the term "integuments" also includes those tissues, such as endothelium, which are derived therefrom. By "embryogenic" is meant the capability of cells to develop into an embryo under permissive conditions. It will be appreciated that the term "in an active form" includes proteins which are truncated or otherwise mutated with the proviso that they initiate or amplify embryogenesis whether or not in doing this they interact with the signal transduction components that they otherwise would in the tissues in which they are normally present.

The term "plant material" includes protoplasts, isolated plant cells (such as stomatal guard cells) possessing a cell wall, pollen, whole tissues such as emerged radicle, stem, leaf, petal,

hypocotyl section, apical meristem, ovaries, zygotic embryo *per se*, roots, vascular bundle, pericycle, anther filament, somatic embryos and the like.

A further embodiment of the invention relates to a DNA molecule comprising a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic.

The said nucleotide sequence may be introduced into the plant material, *inter alia*, via a bacterial or viral vector, by micro-injection, by co-incubation of the plant material and sequence in the presence of a high molecular weight glycol or by coating of the sequence onto the surface of a biologically inert particle which is then introduced into the material.

Expression of the sequence may yield a protein kinase capable of spanning a plant cell membrane. Typically the kinase may be a leucine rich repeat receptor like kinase which has the capacity to auto-phosphorylate. The skilled man will recognize what is meant by the term "leucine rich repeat receptor like kinase". Examples of such proteins include *Arabidopsis* RLK5 (Walker, 1993), *Arabidopsis* RPS2 (Bent *et al.* 1994), Tomato CF-9 gene product (Jones *et al.* 1994), Tomato N (Whitham *et al.* 1994), *Petunia* PRK1 (Mu *et al.* 1994), the product of the *Drosophila* Toll gene (Hashimoto *et al.* 1988), the protein kinase encoded by the rice OsPK10 gene (Zhao *et al.* 1994), the translation product of the rice EST clone ric2976 and the product of the *Drosophila* Pelle gene (Shelton and Wasserman, 1993). Still further examples of such proteins include the TMK1, Clavatal, Erecta, and TMKL1 gene products from *Arabidopsis*, the Flightless-1 gene product from *Drosophila*, the TrkC gene product from pig, the rat LhCG receptor and FSH receptor, the dog TSH receptor, and the human Trk receptor kinase. The protein may comprise a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain. In many receptor kinases the extracellular (ligand binding) domain serves as an inhibitor of the kinase domain in the ligand-free state. This arrest is removed after binding of the ligand. Accordingly, in one embodiment of the invention the protein either lacks a ligand binding domain or the domain is functionally inactivated so that the kinase domain can be constitutively active in the absence of an activating signal (ligand). Whether or not the protein possesses a ligand binding domain - functional or otherwise, once expressed and incorporated into the plant cell membrane the protein binding domain is preferably located intra-cellularly.

In a preferred embodiment of the method, the said sequence further encodes a cell membrane targeting sequence. The sequence may be that which is depicted in SEQ ID Nos. 1, 2, 20, or 32, or it may be similar in that it is complementary to a sequence which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity. By "similar" is meant a sequence which is complementary to a test sequence which is capable of hybridizing to the inventive sequence. When the test and inventive sequences are double stranded the nucleic acid constituting the test sequence preferably has a TM within 20°C of that of the inventive sequence. In the case that the test and inventive sequences are mixed together and denatured simultaneously, the TM values of the sequences are preferably within 10°C of each other. More preferably the hybridization is performed under stringent conditions, with either the test or inventive DNA preferably being supported. Thus either a denatured test or inventive sequence is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of between 50 and 70°C in double strength citrate buffered saline (SSC) containing 0.1%SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SSC concentration. Depending upon the degree of stringency required, and thus the degree of similarity of the sequences, at a particular temperature, - such as 60°C, for example - such reduced concentration buffers are typically single strength SSC containing 0.1%SDS, half strength SSC containing 0.1%SDS and one tenth strength SSC containing 0.1%SDS. Sequences having the greatest degree of similarity are those the hybridization of which is least affected by washing in buffers of reduced concentration. It is most preferred that the test and inventive sequences are so similar that the hybridization between them is substantially unaffected by washing or incubation in one tenth strength sodium citrate buffer containing 0.1%SDS.

Accordingly, further comprised by the present invention is a DNA sequence as depicted in SEQ ID NOS: 22, 24, 26, 28 and 30 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.

The sequence may be modified in that known mRNA instability motifs or polyadenylation signals may be removed and/or codons which are preferred by the plant into which the sequence is to be inserted may be used so that expression of the thus modified sequence in the said plant may yield substantially similar protein to that obtained by expression of the unmodified sequence in the organism in which the protein is endogenous.

In order to obtain expression of the sequence in the regenerated plant (and in particular the carpel thereof) in a tissue specific manner the sequence is preferably under expression control of an inducible or developmentally regulated promoter, typically one of the following: a promoter which regulates expression of SERK genes *in planta*, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* AtDMC1 promoter, the pTA7001 inducible promoter. The DcEP3-1 gene is expressed transiently during inner integument degradation and later in cells that line the inner part of the developing endosperm. The AtChitIV gene is transiently expressed in the micropylar endosperm up to cellularisation. The LTP-1 promoter is active in the epidermis of the developing nucellus, both integuments, seed coat and early embryo. The bel-1 gene is expressed in the developing inner integument and the fbb-7 promoter is active during embryo sac development. The *Arabidopsis* ANT gene is expressed during integument development, and the O126 gene from *Phalaenopsis* is expressed in the mature ovule.

It is most preferred that the sequence is expressed in the somatic cells of the embryo sac, ovary wall, nucellus, or integuments.

The endosperm within the apomictic seed results from fusion of polar nuclei within the embryo sac with a pollen-derived male gamete nucleus. It is preferred that the sequence encoding the protein is expressed prior to fusion of the polar nuclei with the male gamete nucleus.

The invention further includes a DNA, but preferably a recombinant DNA, comprising a sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic. Preferred is a DNA encoding a protein which is a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain, the ligand binding domain optionally being absent or functionally inactive.

In particular, the invention embodies a DNA comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Gln Ser Thr Asp Pro Thr Leu Val Asn Pro Cys Thr Thr Phe His Val Thr Cys Asn.

A specific embodiment of the invention relates to a DNA comprising a DNA sequence encoding a protein having the sequence depicted in SEQ ID Nos. 3 or 21, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity. By substantially similar is meant a pure protein having an amino acid sequence which is at least 90% similar to the sequence of the proteins depicted in SEQ ID No 3 below. In the context of the present invention, two amino acid sequences with at least 90% similarity to each other have at least 90% identical or conservatively replaced amino acid residues in a like position when aligned optimally allowing for up to 8 gaps with the proviso that in respect of each gap a total not more than 4 amino acid residues is affected. For the purpose of the present invention conservative replacements may be made between amino acids within the following groups:

- (i) Serine and Threonine;
- (ii) Glutamic acid and Aspartic acid;
- (iii) Arginine and Lysine;
- (iv) Asparagine and Glutamine;
- (v) Isoleucine, Leucine, Valine and Methionine;
- (vi) Phenylalanine, Tyrosine and Tryptophan
- (vii) Alanine and Glycine

In addition, non-conservative replacements may also occur at a low frequency. Accordingly, the invention further embodies a DNA comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn, with Xaa being a variable amino acid, but preferably Leu or Val.

Especially preferred within the scope of the invention is a DNA comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Xab Xac Xad Xae Val Xaf Arg Val Asp Leu Gly Asn Xag Xah Leu Ser Gly His Leu Xai Pro Glu Leu Gly Xaj Leu Xak Xal Leu Gln, with Xaa to Xak representing variable amino acids, but preferably

Xaa = Leu or Val

Xab = Asn or Gln

Xac = Glu or Asp or His

Xad = Asn or His

Xae = Ser or Arg or Gln

Xaf = Ile or Thr

Xag = Ala or Ser

Xah = Glu or Asn

Xai = Val or Ala

Xaj = Val or Lys

Xak = Lys or Glu

Xal = Asn or His

It is preferred that the DNA further encodes a cell membrane targeting sequence, and that the protein encoding region is under expression control of a developmentally regulated or inducible promoter, such as, for example, a promoter which regulates expression of SERK genes *in planta*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, or the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* AtDMC1 promoter, or the pTA7001 inducible promoter.

Particularly preferred embodiments of the said DNA include those depicted in SEQ ID Nos. 1, 2, 20 or 32, or those which are complementary to one which hybridizes under stringent conditions with the said sequences and which encode a membrane bound protein having kinase activity. As indicated above, the DNA may be modified in that known mRNA instability motifs or polyadenylation signals may be removed and/or codons which are preferred by the plant into which the DNA is to be inserted may be used so that expression of the thus modified DNA in the said plant may yield substantially similar protein to that obtained by expression of the unmodified DNA in the organism in which the protein is endogenous.

The invention still further includes a vector which contains DNA as indicated in the three immediately preceding paragraphs, plants transformed with the recombinant DNA or vector, and the progeny of such plants which contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny.

The recombinant DNA molecules of the invention can be introduced into the plant cell in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of plant, i.e. monocot or dicot, targeted for transformation. Suitable methods of transforming plant cells include microinjection

(Crossway et al., *BioTechniques* 4:320-334 (1986)), electroporation (Riggs et al, *Proc. Natl. Acad. Sci. USA* 83:5602-5606 (1986), *Agrobacterium* mediated transformation (Hinchee et al., *Biotechnology* 6:915-921 (1988)), direct gene transfer (Paszkowski et al., *EMBO J.* 3:2717-2722 (1984)), ballistic particle acceleration using devices available from Agracetus, Inc., Madison, Wisconsin and Dupont, Inc., Wilmington, Delaware (see, for example, Sanford et al., U.S. Patent 4,945,050; and McCabe et al., *Biotechnology* 6:923-926 (1988)), and protoplast transformation/regeneration methods (see U.S. Patent No. 5,350,689 issued Sept. 27, 1994 to Ciba-Geigy Corp.). Also see, Weissinger et al., *Annual Rev. Genet.* 22:421-477 (1988); Sanford et al., *Particulate Science and Technology* 5:27-37 (1987)(onion); Christou et al., *Plant Physiol.* 87:671-674 (1988)(soybean); McCabe et al., *Bio/Technology* 6:923-926 (1988)(soybean); Datta et al., *Bio/Technology* 8:736-740 (1990)(rice); Klein et al., *Proc. Natl. Acad. Sci. USA*, 85:4305-4309 (1988)(maize); Klein et al., *Bio/Technology* 6:559-563 (1988)(maize); Klein et al., *Plant Physiol.* 91:440-444 (1988)(maize); Fromm et al., *Bio/Technology* 8:833-839 (1990); and Gordon-Kamm et al., *Plant Cell* 2:603-618 (1990)(maize).

Comprised within the scope of the present invention are transgenic plants, in particular transgenic fertile plants transformed by means of the aforescribed processes and their asexual and/or sexual progeny, which still contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny.

The transgenic plant according to the invention may be a dicotyledonous or a monocotyledonous plant. Such plants include field crops, vegetables and fruits including tomato, pepper, melon, lettuce, cauliflower, broccoli, cabbage, brussels sprout, sugar beet, corn, sweetcorn, onion, carrot, leek, cucumber, tobacco, alfalfa, aubergine, beet, broad bean, celery, chicory, cow pea, endive, gourd, groundnut, papaya, pea, peanut, pineapple, potato, safflower, snap bean, soybean, spinach, squashes, sunflower, sorghum, water-melon, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. In a preferred embodiment, the DNA is expressed in "seed crops" such as corn, sweet corn and peas etc. in such a way that the apomictic seed which results from such expression is not physically mutated or otherwise damaged in comparison with seed

from untransformed like crops. Preferred are monocotyledonous plants of the Graminaceae family involving Lolium, Zea, Triticum, Triticale, Sorghum, Saccharum, Bromus, Oryzae, Avena, Hordeum, Secale and Setaria plants.

More preferred are transgenic maize, wheat, barley, sorghum, rye, oats, turf and forage grasses, millet and rice. Especially preferred are maize, wheat, sorghum, rye, oats, turf grasses and rice.

Among the dicotyledonous plants *Arabidopsis*, soybean, cotton, sugar beet, sugar cane, oilseed rape, tobacco and sunflower are more preferred herein. Especially preferred are soybean, cotton, tobacco, sugar beet and oilseed rape.

The expression 'progeny' is understood to embrace both, "asexually" and "sexually" generated progeny of transgenic plants. This definition is also meant to include all mutants and variants obtainable by means of known processes, such as for example cell fusion or mutant selection and which still exhibit the characteristic properties of the initial transformed plant, together with all crossing and fusion products of the transformed plant material. This also includes progeny plants that result from a backcrossing, as long as the said progeny plants still contain the DNA according to the invention

Another object of the invention concerns the proliferation material of transgenic plants.

The proliferation material of transgenic plants is defined relative to the invention as any plant material that may be propagated sexually or asexually *in vivo* or *in vitro*. Particularly preferred within the scope of the present invention are protoplasts, cells, calli, tissues, organs, seeds, embryos, pollen, egg cells, zygotes, together with any other propagating material obtained from transgenic plants.

Parts of plants, such as for example flowers, stems, fruits, leaves, roots originating in transgenic plants or their progeny previously transformed by means of the process of the invention and therefore consisting at least in part of transgenic cells, are also an object of the present invention. Espeically preferred a apomictic seeds.

A further object of the invention is a method of producing apomictic seeds, but preferably seeds that are of the adventitious embryony type, comprising the steps of:

- (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell

embryogenic, but preferably a protein which is a protein kinase capable of spanning a plant cell membrane and capable of autophosphorylation.

(ii) regenerating the thus transformed material into plants, or carpel-containing parts thereof, and

(iii) expressing the sequence in the vicinity of the embryo sac.

The kinase protein being expressed by the DNA according to the invention is preferably a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain. In a specific embodiment of the invention, the said kinase protein may lack a functional ligand binding domain but comprises a proline box, a transmembrane domain, a kinase domain and a protein binding domain.

The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction or vegetative growth and can thus be maintained and propagated in progeny plants. Generally said maintenance and propagation make use of known agricultural methods developed to fit specific purposes such as tilling, sowing or harvesting. Specialized processes such as hydroponics or greenhouse technologies can also be applied. As the growing crop is vulnerable to attack and damages caused by insects or infections as well as to competition by weed plants, measures are undertaken to control weeds, plant diseases, insects, nematodes, and other adverse conditions to improve yield. These include mechanical measures such as tillage of the soil or removal of weeds and infected plants, as well as the application of agrochemicals such as herbicides, fungicides, gametocides, nematicides, growth regulants, ripening agents and insecticides.

Use of the advantageous genetic properties of the transgenic plants and seeds according to the invention can further be made in plant breeding which aims at the development of plants with improved properties such as tolerance of pests, herbicides, or stress, improved nutritional value, increased yield, or improved structure causing less loss from lodging or shattering. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding,

variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pestidice treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

In seeds production germination quality and uniformity of seeds are essential product characteristics, whereas germination quality and uniformity of seeds harvested and sold by the farmer is not important. As it is difficult to keep a crop free from other crop and weed seeds, to control seedborne diseases, and to produce seed with good germination, fairly extensive and well-defined seed production practices have been developed by seed producers, who are experienced in the art of growing, conditioning and marketing of pure seed. Thus, it is common practice for the farmer to buy certified seed meeting specific quality standards instead of using seed harvested from his own crop. Propagation material to be used as seeds is customarily treated with a protectant coating comprising herbicides, insecticides, fungicides, bactericides, nematicides, molluscicides or mixtures thereof. Customarily used protectant coatings comprise compounds such as captan, carboxin, thiram (TMTD<sup>®</sup>), methalaxyl (Apron<sup>®</sup>), and pirimiphos-methyl (Actellic<sup>®</sup>). If desired these compounds are formulated together with further carriers, surfactants or application-promoting adjuvants customarily employed in the art of formulation to provide protection against damage caused by bacterial, fungal or animal pests. The protectant coatings may be applied by impregnating propagation material with a liquid formulation or by coating with a combined wet or dry formulation. Other methods of application are also possible such as treatment directed at the buds or the fruit.

It is thus a further object of the present invention to provide plant propagation material for cultivated plants, but especially plant seed that is treated with an seed protectant coating customarily used in seed treatment.

It is a further aspect of the present invention to provide new agricultural methods such as the methods exemplified above which are characterized by the use of transgenic plants, transgenic plant material, or transgenic seed according to the present invention.

To breed progeny from plants transformed according to the method of the present invention, a method such as that which follows may be used: plants produced as described in the examples set forth below are grown in pots in a greenhouse or in soil, as is known in the art, and permitted to flower. Pollen is obtained from the mature stamens and used to pollinate the pistils of the same plant, sibling plants, or any desirable plant. Similarly, the pistils developing on the transformed plant may be pollinated by pollen obtained from the same plant, sibling plants, or any desirable plant. Transformed progeny obtained by this method may be distinguished from non-transformed progeny by the presence of the introduced gene(s) and/or accompanying DNA (genotype), or the phenotype conferred. The transformed progeny may similarly be selfed or crossed to other plants, as is normally done with any plant carrying a desirable trait. Similarly, tobacco or other transformed plants produced by this method may be selfed or crossed as is known in the art in order to produce progeny with desired characteristics. Similarly, other transgenic organisms produced by a combination of the methods known in the art and this invention may be bred as is known in the art in order to produce progeny with desired characteristics.

Further comprised by the invention is a method of obtaining embryogenic cells in plant material, comprising transforming the material with a recombinant DNA sequence or a vector according to the invention, expressing the sequence in the material or derivatives thereof and subjecting the said material or derivatives to a compound which acts as a ligand for the gene product of the said sequence.

The invention further relates to a method of generating somatic embryos under *in vitro* conditions wherein the SERK protein is overexpressed ectopically.

The invention still further includes the use of the said DNA in the manufacture of apomictic seeds, in which use the sequence is expressed in the vicinity of the embryo sac.

In a specific embodiment of the invention the SERK gene may be expressed in transgenic plants such as, for example, an *Arabidopsis* plant, under the control of plant expression signals, particularly a promoter which regulates expression of SERK genes *in planta*, but preferably a

developmentally regulated or inducible promoter such as, for example, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, or the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* AtDMC1 promoter, or the pTA7001 inducible promoter.

The promoters of the DcEP3-1 and the AtChit IV genes may be cloned and characterized by standard procedures. The DcSERK coding sequence (SEQ ID No. 2) is cloned behind the DcEP3-1, the AtChit IV or the AtLTP-1 promoters and transformed into *Arabidopsis*. The ligation is performed in such a way that the promoter is operably linked to the sequence to be transcribed. This construct, which also contains known marker genes providing for selection of transformed material, is inserted into the T-DNA region of a binary vector such as pBIN19 and transformed into *Arabidopsis*. Agrobacterium-mediated transformation into *Arabidopsis* is performed by the vacuum infiltration or root transformation procedures known to the skilled man. Transformed seeds are selected and harvested and (where possible) transformed lines are established by normal selfing. Parallel transformations with 35S promoter-SERK constructs and the entire SERK gene itself are used as controls to evaluate over-expression in many cells or only in the few cells that naturally express the SERK gene. The 35S promoter-SERK construct may give embryo formation wherever the signal that activates the SERK-mediated transduction chain is present in the plant. A testing system based on emasculation and the generation of donor plant lines for pollen carrying LTP1 promoter-GUS and SERK promoter-barnase is established.

The same constructs (35S, EP3-1, AtChitIV, AtLTP-1 and SERK promoters fused to the SERK coding sequence) are employed for transformation into several *Arabidopsis* backgrounds. These backgrounds are wild type, male sterile, fis (allelic to emb 173) and primordia timing (pt)-1 lines, or a combination of two or several of these backgrounds. The wt lines are used as a control to evaluate possible effects on normal zygotic embryogenesis, and to score for seed set without fertilization after emasculation. The ms lines are used to score directly for seed set without fertilization. The fis lines exhibit a certain degree of seed and embryo development without fertilization, so may be expected to have a natural tendency for apomictic embryogenesis, which may be enhanced by the presence of the SERK constructs. The pt-1 line has superior regenerative capabilities and has been used to initiate the first stably embryogenic *Arabidopsis* cell suspension cultures. Combinations of several of the above backgrounds are obtained by

crossing with each other and with lines containing ectopic SERK expressing constructs. Except for the ms lines, propagation can proceed by normal selfing, and analysis of apomictic traits following emasculation. A similar strategy is followed in which the ATChlV, AtLTP-1 and SERK promoters are replaced by the *bel-1* and *fbp-7* promoters as well by other promoters specific for components of the female gametophyte.

Additional constructs are generated that have constitutive receptor kinase activity. Most of the receptor kinases of the SERK type act as homodimeric receptors, requiring autophosphorylation before being able to activate downstream signal transduction cascades. In many receptor kinases the extracellular domain serves as an inhibitor of the kinase domain in the ligand-free stage. This arrest is removed after binding of the ligand (Cadena and Gill, 1992). By introduction of a SERK construct, from which the extracellular ligand-binding domain has been removed, mutant homodimeric (in cells that do not have a natural population of SERK proteins) or heterodimeric (in cells that also express the unmodified forms) proteins can be generated with a constitutively activated kinase domain. This approach, when coupled to one of the promoters active in the nucellar region, results in activation of the embryogenic pathway in the absence of the activating signal. This may be an important alternative in cases where it is necessary or desirable to have activation of the SERK pathway only dependant on specific promoter activity and independent of temporal regulation of an activating signal. Introduction of SERK constructs that result in fertilization-independent-embryogenesis (*fie*) are tested in other species for their effect. In order to recognize the *fie* phenotype, the skilled man will use appropriate male sterile backgrounds. However, pollination is often necessary for apomixis of the adventitious embryo type, in order to ensure the production of endosperm.

Whilst the present invention has been particularly described by way of the production of apomictic seed by heterologous expression of the SERK gene in the nucellar region of the carpel, the skilled man will recognize that other genes, the products of which have a similar structure/function to the SERK gene product, may likewise be expressed with similar results. Moreover, although the example illustrates apomictic seed production in *Arabidopsis*, the invention is, of course, not limited to the expression of apomictic seed-inducing genes solely in this plant. Moreover, the present disclosure also includes the possibility of expressing the SERK (or related) gene sequences in the transformed plant material in a constitutive - tissue non-specific manner (for example under transcriptional control of a CaMV35S or NOS promoter). In this case, tissue specificity is assured by the localized presence within the vicinity of the embryo

sac of the ligand of the product of the said gene. Furthermore, the SERK (or related) gene products may interact with proteins such as transcription factors which are involved in regulating embryogenesis. This interaction within tissue which has been transformed according to the present disclosure is also part of the present invention.

The skilled man who has the benefit of the present disclosure will also recognize that the SERK gene (and others as indicated in the preceding paragraph) may be transformed into plant material which may be propagated and/or differentiated and used as an explant from which somatic embryos can be obtained. Expression of such sequences in the transformed tissue (which is subjected to a ligand of the kinase gene products) substantially increases the percentage of the cells in the tissue which are competent to form somatic embryos, in comparison with the number present in non-transformed like tissue.

The invention will be further apparent from the following description and the associated drawings and sequence listings.

SEQ ID NO. 1 depicts the *Daucus carota* genomic clone of the putative receptor kinase (SERK) associated with the transition of competent to embryogenic cells;

SEQ ID NO. 2 depicts the cDNA of the said putative kinase;

SEQ ID NOs. 3 depicts the predicted protein sequence of the SERK protein encoded by the DNA of SEQ ID NO:1.

SEQ ID NOs: 4-16 depict the sequences of various PCR primers; and

SEQ ID NOs. 17-19 depict specific peptides contained within the gene product of SEQ ID NO. 2.

SEQ ID NO: 20 depicts the *Arabidopsis thaliana* partial genomic clone of the putative receptor kinase (SERK) associated with the transition of competent to embryogenic cells.

SEQ ID NO: 21 depicts the predicted protein sequence of the SERK protein encoded by the DNA of SEQ ID NO:20.

SEQ ID NOs: 22, 24, 26, 28 and 30 depict the partial DNA sequences of 5 EST clones with high homology to the SERK LRR sequences .

SEQ ID NOs. 23, 25, 27, 29 and 31 depict the predicted protein sequence of the partial DNA sequences of the 5 EST clones of SEQ ID Nos: 22, 24, 26, 28 and 30.

SEQ ID NO: 32 depicts the nucleotide sequence of the SERK cDNA from *Arabidopsis thaliana*.

SEQ ID NO: 33 depicts the predicted amino acid sequence of the SERK protein from *Arabidopsis thaliana* encoded by the DNA of SEQ ID NO: 32.

Figure 1 shows the results of an RT-PCR experiment performed on RNA extracted from the indicated tissues. 40 cycles followed by Southern blotting of the resulting bands is necessary to visualize SERK expression. Lanes include explants at day 7, treated for less (lane 1) or more (lane 2) than 3 days with 2,4-D. In the original a very faint signal is visible in lane 2, but not in lane 1. Established embryogenic cultures (lanes 4-6) but not a non-embryogenic control (lane 3) express the SERK gene. In carrot plants, no expression is detectable except for developing seeds after pollination (lane 7). Up to day 7 after pollination, the carrot zygote remains undivided, suggesting that the observed signal is coming only from the zygote. At day 10, the early globular and at day 20 the heart stage is reached in carrot zygotic embryogenesis. No signals are seen on Northern blots.

Figure 2A shows the results of a whole-mount *in situ* hybridization with the SERK cDNA on 7 day explants treated for 3 days with 2,4 D. Few cells on the surface of the explant express the SERK gene, and those cells that do are the ones that become embryogenic. Figure 2B shows a whole mount *in situ* hybridization on a partially dissected seed containing a globular zygotic embryo. Hybridization is visualized by DIG staining.

Figure 3 shows SERK expression in embryogenic hypocotyl cells during hormone-induced activation, determined by whole mount *in situ* hybridization . Bar: 50 mm

(A-E) Cell population generated by mechanical fragmentation of the activated hypocotyls. Only few of a certain type of cell, defined enlarged cell show SERK expression (asterisks). Small cytoplasmic cells (c), enlarging cells (eg) and large cells (!) never show SERK expression.

(F) Hypocotyl longitudinal section before hormone-induced activation. It is not possible to detect any SERK expression in any type of cell.

(G-I) Proliferating mass coming from the inner hypocotyl tissues 10 days after the beginning of the hormonal treatment (longitudinal section). In G a single enlarged cells showing SERK expression is detectable within a row of negative cells showing the same morphology. In H a single enlarged cell showing serk expression is detaching from the surface of the proliferating mass. In I a cluster of enlarged cells showing SERK expression is detectable at the surface of proliferating tissue.

(J) Proliferating mass coming from the inner tissues of the hypocotyl 10 days after the beginning of the rooting treatment (24 hours with 2,4-D followed by hormone removal). Both the root primordia and the enlarged cells detaching from the surface do not show any SERK expression.

Figure 4 shows the phenotype of *Arabidopsis* WS plants transformed with the 2200 bp SERK-luciferase construct at the seedling level. Pictures were taken at 28 days after germination of T2 seeds. In plant II and III no clear shoot meristem is visible at the seedling stage, 7 days after germination. The first two leaves, if they develop at all, are needle-shaped as shown on the pictures taken 28 days after germination. At this time plant I, which shows no clear phenotype, already starts flowering. Secondary shoot meristems are already developing in plant no II and will also develop later from no III. Shoot meristems, inflorescences and normal flowers eventually develop on all plants.

Figure 5 shows how the 2200 bp SERK luciferase construct affects the number of developing ovules in the siliques of transformed plants.

Figure 6 shows autophosphorylation of purified SERK fusion protein *in vitro*. Lane 1: purified SERK fusion protein; Lane 2: serine phosphate; Lane 3: threonine phosphate; Lane 4: tyrosine phosphate.

The following description illustrates the isolation and cloning of the SERK gene and the production of apomictic seed by heterologous expression of the said gene in the nucellar region of the carpel so that somatic embryos form which penetrate the embryo sac and are encapsulated by the seed as it develops.

## ISOLATION AND CLONING OF THE SERK GENE FROM DAUCUS CAROTA

### **Isolation of cDNA clones that are preferentially expressed in embryogenic cell cultures of carrot**

In order to increase the chance of success for obtaining genes expressed in carrot suspension cells competent to form embryos, the number of embryo-forming cells as present in a series of established cell cultures was determined. A sub-population of cells that passed through a 30 mm nylon sieve was isolated from eight different cultures that ranged in age between 2 months and 4 years. In these sub 30 mm populations, the number of embryos formed from the single cells and small cell clusters was determined and expressed as a percentage of the total number of cells present at the start of embryogenesis. Sieved <30 mm cultures able to form somatic embryos with a frequency of more than 1% were then used as a source for competent cells, and cultures that produced less than 0.01% embryos were used as non-embryogenic controls. As main cloning strategies, cold plaque screening (Hodge et al. 1992) and differential display (dd) RT-PCR (Liang and Pardee, 1992) were used besides conventional differential screening of cDNA libraries.

Labeled probes for differential screening were obtained from RNA out of a <30 mm sieved sub-population of cells from either embryogenic or non-embryogenic cell cultures. Employing these probes in a library screen of approximately 2000 plaques yielded 26 plaques that failed to show any hybridization to either probe. These so-called cold plaques were purified and used for further analysis. From the total number of plaques that did hybridize, about 30 did so only with the probe from embryogenic cells. ddRT-PCR reactions using a combination of one anchor primer and one decamer primer were performed on mRNA isolated from three embryogenic, and three non-embryogenic suspension cultures. About 50 different ddRT-PCR fragments were obtained from each reaction. Using combinations of three different anchor and six different decamer primers, a total of approximately 1000 different cDNA fragments was visualized. Six of these PCR fragments were only found in lanes made with mRNA from <30 mm populations of cells from embryogenic cultures (Table 1) and with oligo combinations of the anchor primer (5'-TTTTTTTTTGC-3') and the decamer primers (5'-GGGATCTAAG-3'), (5'-ACACGTGGTC-3'), (5'-TCAGCACAGG-3'). Because differential PCR fragments often consist of several unresolved cDNA fragments (Li et al. 1994), cloning proved to be essential prior to undertaking further characterization of the PCR fragments obtained.

All clones obtained were subjected to a second screen, that consisted of spot-dot Northern hybridization performed under conditions of high stringency. This method, that used RNA from entire unsieved embryogenic and non-embryogenic suspension cultures, proved to be a fast and reliable additional selection method. Only one clone (22-28) of the 30 clones obtained after differential screening, proved to be restricted to embryogenic cell cultures while the majority was constitutively expressed. The 26 clones obtained from the cold plaque screening required long exposure times in the spot-dot Northern analysis. Six of these clones failed to show any hybridization signal and 19 proved to be expressed in both embryogenic and non-embryogenic cell cultures. One clone (31-50) showed low expression in all embryogenic cultures, and in one non-embryogenic culture, but not in the others. Of the six cloned fragments obtained by ddRT-PCR display, four showed hybridization more or less restricted to transcripts present in embryogenic cultures. All clones that passed through the second screening were sequenced. Two of the ddRT-PCR clones (6-8 and 7-13) were identical to the carrot Lipid Transfer Protein (LTP) gene, previously identified as a marker for embryogenic carrot cell cultures. LTP expression is restricted to embryogenic cell clusters and the protoderm of somatic and zygotic embryos from the early globular stage onwards (Sterk *et al.* 1991). Therefore, while the LTP gene is not a marker for competent cells, its appearance in the screening confirms the validity of our methods with respect to the cloning of genes expressed early during somatic embryogenesis.

#### cDNA clone 31-50 encodes a leucine-rich repeat containing receptor-like kinase

The mRNA corresponding to the isolated clone 31-50 had an open reading frame of 1659 nucleotides encoding a protein with a calculated Mw of 55 kDa. Because clone 31-50 is mainly expressed in embryogenic cell cultures it was renamed Somatic Embryogenesis Receptor Kinase (SERK). The SERK protein contains a N-terminal domain with a five-times repeated leucine-rich motif that is proposed to act as a protein-binding region in LRR receptor kinases (Kobe and Deisenhofer, 1994). Between the extracellular LRR domain of SERK and the membrane-spanning region is a 33 amino acid region rich in prolines (13), that is unique for the SERK protein. Of particular interest is the sequence SPPPP, that is conserved in extensins, a class of universal plant cell wall proteins (Vamer and Lin, 1989). The proposed intracellular domain of the protein contains the 11 subdomains characteristic of the catalytic core of protein kinases. The core sequences HRDVKAAN and GTLGYIAPE in respectively the kinase subdomains VB and VIII suggest a function as a serine / threonine kinase (Hanks *et al.* 1988).

Another interesting feature of the intracellular part of the SERK protein is that the C-terminal 24 amino-acids resembles a single LRR. The serine and threonine residues present within the intracellular LRR sequence are surrounded by acidic residues and might be targets for the autophosphorylation of SERK, thereby regulating the ability of other proteins to interact with this receptor-kinase in a similar fashion as described for the SH2 domain of the EGF family of tyrosine receptor kinases.

Hybridization of the SERK cDNA clone to the carrot genome revealed the presence of only a single main hybridizing band after digestion with EcoR1, probably reflecting a single SERK gene in the carrot genome. This was confirmed after digestion with Ddel, an enzyme that cuts three times within the SERK gene. No signal was observed after Northern blotting of mRNA from embryogenic cell cultures and hybridization with labeled SERK probes, reflecting the low levels of transcript present in these cultures. Detection of the SERK transcript on the original spot-dot Northerns was only possible after long exposure times compared with other probes.

The ability of the SERK protein to autophosphorylate was investigated *in vitro*, using a previously described autophosphorylation assay (Mu et al. 1994), with a bacterial fusion protein that contained the complete intracellular region of the SERK protein. The bacterially expressed SERK fusion protein was able to autophosphorylate, indicating that the SERK protein is able to fulfill a role as a protein kinase *in vivo* (Heldin, 1995).

#### **Expression of the SERK gene corresponds with the first appearance of competent cells during hypocotyl activation**

When carrot hypocotyls are induced with 2,4-D, only the cells of the provascular tissue proliferate. Cells of epidermal and cortical origin merely expand, suggesting that the provascular tissue derived cells form the newly initiated suspension culture. After removal of 2,4-D, the formation of somatic embryos occurs after 2-3 weeks. Somatic embryos are preceded by embryogenic cells, that are developed in turn from competent cells. While competent and embryogenic cell formation take place in the presence of 2,4-D, it was not clear when this occurred, and which cells acquired competence. Since previous experiments (Toonen et al. 1994) revealed that cell morphology is not a good criterion, the first appearance of single competent cells was determined experimentally by semi-automatic cell tracking performed on large populations of immobilized cells. Hypocotyl explants activated with 2,4-D for seven days were mechanically fragmented and samples of the resulting population of mainly single

suspension cells were immobilized to allow recording of their development by cell tracking. In the immobilized cell populations obtained in this way all the morphologically discernible cell types were present that were also seen in the un-fragmented activated hypocotyls. Because the different cell morphologies observed during hypocotyl activation were known (Guzzo et al. 1995), it was possible to trace back the original position of each type of cell in the activated explant. Small cytoplasm-rich cells (16x16 mm) are the proliferating cells that surround the vascular elements. Enlarging vacuolated cells (16x40 mm) are encountered on the surface of the mass of proliferating cells and these can detach from the surface when fully enlarged (35x90 mm). Large vacuolated cells (more than 60x140 mm) are the non-proliferating remnants of the hypocotyl epidermis and cortical parenchyma. The shape of the enlarging and fully enlarged cells could change from oval to elongate or triangular. Cell tracking on a total of 24,722 cells released from seven days activated hypocotyls showed that only 20 single cells formed a somatic embryo. Because of their dependence on continued 2,4-D treatment, the embryo-forming single cells are still in the competent cell stage. All of the embryo-forming single cells belonged to the category of 3,511 enlarged cells, that contained therefore competent cells in a frequency of 0.56%. The single cell tracking experiments clearly reveal that the ability of explant cells to reinitiate cell division under the influence of 2,4-D, resulting in a population of highly cytoplasmic and rapidly proliferating cells, does have a causal relation with the ability to become embryogenic. It is also clear that only a very limited number of the cells that make up the newly initiated embryogenic suspension culture are actually competent to form embryogenic cells.

Expression of the SERK gene, determined by whole mount *in situ* hybridization on a similar population of cells as used for the cell tracking experiments, was found to be restricted to only 0.44% of the enlarged cells. Therefore, the expression of the SERK gene appears closely correlated both qualitatively and quantitatively with the presence of competent single cells.

To obtain insight into the temporal regulation of SERK expression in the course of explant activation, whole mount *in situ* hybridization was performed on entire intact or hand-sectioned explants treated for different periods with 2,4-D. Representative samples were collected at daily intervals from explants untreated and treated for three days, six days, seven days or ten days with 2,4-D before returning to B5-0. No SERK-expressing cells were ever found in explants treated for less than three days with 2,4-D. While enlarged cells became present after the first five days of culture, the first few SERK-expressing enlarged cells were found after six-seven days of culture in the presence of 2,4-D treatment. These few cells were present at the surface

of the mass of proliferating cells originating from the provascular tissue. In the hypocotyls treated for ten days with 2,4-D, the number of SERK-positive cells had increased to 3.04% and included at this stage also cells present in small clusters. No SERK transcript was ever detected in small cytoplasm-rich cells or large vacuolated cells. Hypocotyls were also treated for only one day with 2,4-D and subsequently cultured in hormone-free medium for a total of seven or ten days. Under these conditions explant cells proliferated and gave rise to roots and non-embryogenic cell cultures, while SERK expression could never be detected. The *in situ* hybridization results described above were obtained from a relatively small number of explants and a few hundred cells, so RT-PCR followed by Southern hybridization was performed to obtain more quantitative results. These are shown in Figure 7 and confirm the close temporal correlation between the first appearance of competent cells in explants treated for three days with 2,4-D and the expression of the SERK gene. Northern hybridization never gave any signal after hybridization with SERK cDNA probes, not even after prolonged exposure in a PhosphorImager, in line with the extremely restricted expression pattern of the SERK gene.

**Expression of the SERK gene corresponds with the occurrence of competent cells in established embryogenic cell cultures**

While the results described so far indicate that competent and embryogenic cell formation is restricted to a particular class of enlarged cells during explant activation, the situation in an established embryogenic cell culture is more complex. Competent single cells in such cultures do not appear to belong to one cell type in particular, but have been shown to originate from all morphologically different cell types. In cell tracking experiments, embryogenic cells, that do not require exogenous auxin treatment, were never observed to be single but consisted of clusters of at least 3-4 cells (Toonen et al. 1994). SERK expression was found in all morphologically discernible single cell types that were present in an embryogenic cell culture at a frequency between 0.1 and 0.5% depending on the cell type. In non-embryogenic cultures, SERK expressing cells were never encountered. As was observed in the activated explants, SERK expression was not restricted to single cells, but also occurred in small clusters of 2 to 16 cells. Since clusters of this size are known to consist of embryogenic cells, these data show that SERK expression is not restricted to competent single cells, but may persist in small clusters of embryogenic cells. No SERK expression was encountered during the late globular, heart and torpedo-stages of somatic embryogenesis.

### The SERK gene is transiently expressed in zygotic embryogenesis

The expression of the SERK gene in carrot plants was determined by RT-PCR. The results indicate that no SERK mRNA accumulates in any of the adult plant organs nor in flowers prior to pollination. The first occasion when SERK expression can be detected is in flowers at three days after pollination (DAP), at which stage fertilization has taken place and endosperm development has commenced. SERK mRNA remains present in flowers up to twenty DAP, corresponding with the early globular stage of the zygotic embryo (Yeung et al. 1996). Whole mount *in situ* hybridization on partially dissected carrot seeds confirmed that the SERK gene was only expressed in early embryos up to the globular stage. Expression was observed in the entire embryo including the suspensor. No expression was seen in seedlings, roots, stems, leaves, developing and mature flower organs, pollen grains and stigma's before and after fertilization. Tissues in the developing seed such as seed coat, integuments, all embryo sac constituents before fertilization as well as the endosperm at all stages of development investigated did not show any SERK expression. Later stages of carrot zygotic embryos were also completely devoid of SERK mRNA. Given this pattern of expression, that is restricted to the zygotic embryo, the signal as detected by RT-PCR in flowers at 3 and 7 DAP must come from SERK mRNA as present in zygotes, because in carrot the zygote remains undivided up to one week after pollination (Yeung et al. 1996). Although SERK expression persists to slightly later stages in zygotic globular embryos when compared to the somatic ones, these results confirm the transient pattern of expression as observed for the SERK gene during somatic embryogenesis and also imply that there is a correspondence between the formation of competent cells *in vitro* and the formation of the zygote *in vivo*.

## METHODS

### Cell culture, hypocotyl explant induction and cell tracking

Cell cultures were derived from *Daucus carota* cv. Flakkese and maintained as previously described (De Vries et al. 1988a). Cell suspension cultures were maintained at high cell density in B5 medium (Gamborg et al. 1968) supplemented with 2 mM 2,4-D (B5-2 medium). Embryo cultures with globular, heart and torpedo-stage somatic embryos were derived from <30 mm sieved cell cultures cultured at low cell density (100 000 cells / ml) in B5 medium without 2,4-D (B5-0). For hypocotyl explant induction experiments, plantlets were obtained from seed of

*Daucus carota* cv. S Valery as described previously (Guzzo et al., 1994). The hypocotyls of one week old plantlets were divided in segments of 3-5 mm, incubated for various periods of time in B5-2 medium and returned to B5-0 medium. Seven days after explantation and exposure to 2,4-D the hypocotyl segments were fragmented on a 170 mm sieve and the resulting cells collected to form a fine cell suspension. Immobilization of these cells in B5-0.2 medium was performed in a thin layer of phytigel (Toonen et al. 1994). After one week of further culture 2,4-D was removed by washing the plates with B5-0 medium. This allowed embryos to develop beyond the globular stage. Recording the development of the immobilized cells was performed with a procedure modified from the previously described by Toonen et al. (1994). The main change involved a new MicroScan program for automatic 3-axis movement to scan all cells in the phytigel (Toonen et al. 1996).

#### Nucleic acid isolation and analysis

RNA was isolated from cultured cells and plant tissues as described by De Vries et al. (1988b). Poly(A)<sup>+</sup>-RNA was obtained by purification by oligo (dT) cellulose (Biolabs). For RNA gel blot analysis samples of 10 mg total RNA were electrophoresed on formamide gel, and transferred to nytran-plus membranes. For RNA spot-blot analysis 5 mg of total RNA was denatured and spotted onto nytran-plus filters using a hybridot manifold (BRL).

Genomic DNA was isolated according to Sterk et al. (1991). Samples of 10 mg genomic DNA were digested with different restriction enzymes and separated on agarose gel, and transferred to nytran-plus membrane (Schleicher & Schuell). Hybridization of RNA blots took place at 42°C in hybridization buffer containing 50% formamide, 6xSSC, 5xDenhardt, 0.5% SDS and 0.1 mg/ml salmon sperm DNA. Hybridization of DNA blots was performed as previously described (Sterk et al. 1991). Following hybridization, filters were washed under stringent conditions (3x20 min in 0.1% SSC, 1% SDS, at 65°C). Filters were exposed to Kodak X-Omat AR film. The integrity and the amount of RNA on the blots was confirmed by hybridization with an 18S ribosomal RNA probe. Nucleotide sequence analysis was performed on an ABI 373A automated DNA sequencer (Applied Biosystem).

#### Screening procedures

Two independent cDNA libraries were constructed with equal amounts of poly(A)<sup>+</sup>-RNA from total established cell cultures grown for six days in B5-2 medium, sieved <125 mm cell cultures grown for six days in B5-0 medium and sieved <30 mm cell cultures grown for six days in B5-0

medium. cDNA synthesis and cloning into the Uni-ZAP<sup>TM</sup> XR vector was performed according to the manufacturers protocol (Stratagene).

Differential screening of the cDNA libraries was performed essentially as described by Scott et al. (1991). RNA was isolated from either three embryogenic or three non-embryogenic cell cultures, that were grown for seven days in B5-2 after sieving through 30 mm mesh. First strand cDNA synthesis was performed on 4 mg total RNA using AMV reverse transcriptase (Gibco BRL). [<sup>32</sup>P]dATP labeled probes were prepared using random prime labeling on first strand cDNA. Pooled probes from embryogenic and non-embryogenic cell populations were hybridized to two pairs of nitrocellulose filters, each containing 1000 plaques from one cDNA library. After washing for 3x20 min in 0.1% SSC, 1% SDS at 65°C, hybridization was visualized by autoradiography for two days on Kodak X-omatic film. Plaques that only showed signal with the embryogenic transcript probe were purified by two further rounds of screening.

In order to identify cDNA clones which are expressed at low levels in the <30 mm sieved cell population, cold plaque screening was performed as described by Hodge et al. (1992). Plaques from the differential screening that did not show any signal after seven days of autoradiography were purified by two further rounds of screening. The resulting clones were used as probes for characterization of the expression pattern of the corresponding genes.

#### Differential Display RT-PCR

Differential display of mRNA was performed essentially as described by Liang and Pardee (1992). cDNA synthesis took place by annealing 1 mg of total RNA in 10 ml buffer containing 200 mM KCl, 10 mM Tris-HCl (pH 8.3), and 1 mM EDTA with 100 ng of one of the following anchor primers: (5'-TTTTTTTTTTGC-3'), (5'-TTTTTTTTTTCTG-3'), (5'-TTTTTTTTTTCA-3'). Annealing took place by heating the mix for 3 min. at 83°C followed by incubation for 30 min at 42°C. Annealing was followed by the addition of 15 ml pre-warmed cDNA buffer containing 16 mM MgCl<sub>2</sub>, 24 mM Tris-HCl (pH 8.3), 8 mM DTT, 400 mM dNTP, and 4 Units AMV reverse transcriptase (Gibco BRL). cDNA synthesis took place at 42°C for 90 min. First strand cDNA was phenol/chlorophorm extracted and precipitated with ethanol using glycogen as a carrier. The PCR reaction was performed in a reaction volume of 20 ml containing 10% of the synthesized cDNA, 100 ng of anchor primer, 20 ng of one of the following 10-mer primers: (5'-GGGATCTAAG-3') , (5'-TCAGCACAGG-3'), (5'-GACATCGTCC-3'), (5'-CCCTACTGGT-3'), (5'-ACACGTGGTC-3'), (5'-GGTGACTGTC-3'), 2 mM dNTP, 0.5 Unit Taq enzyme in PCR buffer (10

mM Tris-HCl (pH 9.0), 1.5 mM MgCl<sub>2</sub>, 50 mM KCl, 0.01% gelatin and 0.1% Triton X100) and 6 nM [ $\alpha$ -<sup>32</sup>P] dATP (Amersham). PCR parameters were 94°C for 30 sec, 40°C for 1 min, and 72°C for 30 sec for 40 cycles using a Cetus 9600 (Perkin-Elmer). Amplified and labeled cDNAs were separated on a 6% denaturing DNA sequencing gel. Gels were dried without fixation and bands were visualized by 16 hours of autoradiography using Kodak X-omat film. Bands containing differentially expressed cDNA fragments of 150–450 nucleotides were cut out of the gel and DNA was extracted from the gel slices by electroelution onto DE-81 paper (Whatmann). After washing of the paper in low salt buffer (100 mM LiCl<sub>2</sub> in 10 mM TE buffer), and elution of the cDNA in high salt buffer (1 M LiCl<sub>2</sub> in 10 mM TE buffer with 20% ethanol) the cDNA was concentrated by precipitation in ethanol using glycogen as carrier. Reamplification of the cDNA fragments using the same PCR cycling parameters as described above but PCR buffer containing 2.5 mM of both the 10-mer and the anchor oligo and 100 mM dNTP. DE-81 paper allowed an efficient recovery of the DNA fragments and reamplification generated an average of 500 ng DNA after 40 cycles. Amplified PCR products were blunt-ended using the Klenow fragment of *E.coli* DNA Polymerase I (Pharmacia), purified on Sephadryl-S200 columns (Pharmacia), ligated into a SmaI linearized pBluescript vector II SK (Stratagene) and transformed into *E.coli* using electroporation.

#### RT-PCR

Adult plant tissues from *Daucus carota* were obtained from S&G Seeds (Enkhuizen). Controlled pollination was performed by hand. Flower tissue RNA was obtained from three complete umbels for each time-point and contained all flower organs including pollen grains. 2 mg of total RNA from adult plant tissue or cell cultures was annealed at 42°C with 50 ng oligo (5'-TCTTGGACCAGATAATTTC-3') in 10 ml annealing buffer (250 mM KCl, 10 mM Tris-HCl pH 8.3, 1 mM EDTA). After 30 min. annealing, 1 unit AMV-reverse transcriptase was added in a volume of 15 ml cDNA buffer (24 mM Tris-HCl pH 8.3, 16 mM MgCl<sub>2</sub>, 8 mM DTT, 0.4 mM dNTP). The reverse transcription reaction took place for 90 min. at 42°C. PCR amplification of SERK-cDNA was carried out with two specific oligos for the SERK kinase domain, (5'-CTCTGATGACTTCCAGTC-3') and (5'-AATGGCATTGCATGG-3'). Amplification was carried out with 30 cycles of 30 sec. at 94°C, annealing at 54°C for 30 sec. and extension at 72°C for 1 min., followed by a final extension for 10 min. at 72°C.

### Whole mount *in situ* hybridization

Whole mount *in situ* hybridizations were performed essentially as previously described (Engier et al. 1994). Cell cultures and somatic embryos were immobilized on poly-L-lysine coated glasses during fixation to improve handling. Whole mount *in situ* hybridization on explants took place by embedding hypocotyls from seven-days old plantlets in 3% Seaplaque agarose (Duchefa) and processing them in Eppendorf tubes. Transverse as well as longitudinal sections were made with a vibrotome (Biorad Microcut). Sections of 50-170 mm thick were incubated in B5-2 medium for a minimum of three days to induce formation of embryo-forming cells. Optimal induction was achieved with longitudinal hypocotyl sections with a thickness of at least 90 mm. To obtain proliferating, non-embryogenic cell cultures, hypocotyl sections were exposed to 2,4-D for only 1 day, and subsequently transferred to B5-0 medium (Guzzo et al. 1994). Whole mount *in situ* hybridization on developing seeds was performed by removing the chalazal end of the seeds to allow easier probe penetration. After hybridization, the enveloping layers of integuments and endosperm were carefully removed to expose the developing embryos. *In situ* hybridization on sections was performed as described previously (Sterk et al. 1991) except for the use of non-radioactive probes.

All samples were fixed for 60 min. in PBS containing 70 mM EGTA, 4% paraformaldehyde, 0.25% glutaraldehyde, 0.1% Tween 20, and 10% DMSO. Samples were then washed, treated with proteinase K for 10 min, again washed and fixed a second time. Hybridization solution consisted of PBS containing 0.1% Tween 20, 330 mM NaCl, 50 mg/ml heparin, and 50% deionized formamide. Hybridization took place for 16 hours at 42°C using digoxigenin-labeled sense or antisense riboprobes (Boehringer Mannheim). After washing the cells were treated with RNaseA, and incubated with anti-digoxigenin-alkaline phosphatase conjugate (Boehringer Mannheim) which had been preabsorbed with a plant protein extract. Excess antibody was removed by washing followed by rinsing in staining buffer (100 mM Tris-HCl pH 9.5, 100 mM NaCl, 5 mM MgCl<sub>2</sub>, 1 mM levamisole) and the staining reaction was performed for 16 hours in a buffer containing NBT and BCIP. Observations were performed using a Nikon Optiphot microscope equipped with Nomarski optics.

### Autophosphorylation assay

A 1.4 kB SspI cDNA fragment of the SERK cDNA encoding most of the open reading frame apart from the N-terminal three LRRs was cloned into the pGEX expression vector (Pharmacia).

A fusion protein consisting of SERK and the glutathione S-transferase gene product was synthesized by a three hours induction of transformed *E.coli* with 2 mM IPTG. Fusion protein was isolated and purified as described previously (Horn and Walker, 1994). Purified fusion protein was coupled to glutathione agarose beads (Sigma) and incubated for 20 min. at 20°C in a volume of 10 ml buffer: 50 mM Hepes (pH 7.6), 10 mM MgCl<sub>2</sub>, 10 mM MnCl<sub>2</sub>, 1 mM DTT, 1 mCi [ $\gamma$  -<sup>32</sup>P] (3 000 Ci/mmol). Excess label was removed by washing the fusion protein/glutathione agarose beads three times for 5 min. in 50 mM Tris-HCl (pH 7.3), 10 mM MgCl<sub>2</sub> at 4°C. Protein was removed from the beads by cooking in SDS-PAGE loading buffer. Equal amounts of protein were separated by SDS-PAGE and protein autophosphorylation was visualized by autoradiography.

#### SERK fusion proteins produced with the Baculovirus expression system.

Further fusion proteins containing the intracellular part of the *Daucus carota* SERK protein (1.0 kB HindIII / Sspl fragment of the carrot SERK cDNA clone 31-50) were made using the baculovirus vector pAcHLT.

*In vitro* phosphorylation studies with this purified protein showed that most if not all of the autophosphorylation of this SERK fusion protein was at threonine residues (Figure 6)

#### Construction of viral transfer vectors

The pAcHLT-B and pAcHLT-C baculovirus transfer vectors were used for the cloning of two cDNA fragments of the carrot SERK gene. The Sspl 1.41 kB fragment of carrot DcSERK cDNA was cloned into the SmaI site of pAcHLT-B and the Sspl / Pvull 1.07 kB fragment of carrot DcSERK cDNA was cloned into the SmaI site of pAcHLT-C. The first construct contains the complete C-terminal part of the DcSERK protein and from the putative extracellular region the proline-rich region and three of the leucine-rich repeats. The second construct contains only the putative intracellular region of the DcSERK gene product. Nucleotide sequence analysis was performed in order to confirm the presence and the orientation of the DcSERK cDNA within the vector.

#### Transformation of insect cells

The resulting transfer vectors were used to transfet (lipofect) insect cell culture Sf21 from *Spodoptera frugiperda* in combination with linearized AcMNPV baculovirus DNA. Monolayers of SF21 cells were transfected in 35 mm petridishes containing 2 ml of Hink's

medium. One microgram of linearized AcMNPV baculovirus DNA (Baculogold, Invitrogen) was added to 5 microgram of pAcHLT / SERK vector construct in 25 microliter of water. Fifteen microliter of Lipofectin (BRL) was mixed with 10 microliter of water, after which the DNA solution was added. After mixing 200 microliter of Hink's medium was added to the mix and the solution was transferred to the cell monolayer, from which the medium was removed. After one hour, 500 microliter of Hink's medium was added and the cells were incubated for another 3 hours. Finally, 1 ml of Hink's medium with 20% foetal bovine serum (FBS) was added and the cells were incubated for 4 days. After transfection, the viral infection could be identified by the reduced growth of cells, the swollen shape and the enlarged nucleus. After four days, infected cells were harvested and the medium containing infectious budded virus was collected and used for plaque assays and amplification of recombinant virus stocks.

#### Isolation of single recombinant viruses

Single recombinant virus plaques were isolated from monolayers of cells infected with a titration range of the primary virus stock. Infection was performed in 35 mm petridishes with monolayers of cells. Virus stocks were diluted in 600 microliter of Graces medium and added to the cell monolayer, followed by a 90 minutes incubation period at in Graces medium with 20% FBS. Afterwards, 3% Sea Plaque agarose was autoclaved, mixed with an equal amount of 2x Graces medium with 20% FBS and from the resulting agarose overlay solution 2 ml. was spread over the cell monolayers after removal of the viral inoculum. After 4 days of incubation single plaques could be visualized and purified for further analysis.

#### Fusion protein production.

After determining the titer of purified recombinant viruses, monolayers of Sf21 cells in 75 cm<sup>2</sup> flasks were infected with a multiplicity of infection (MOI) of 10. Incubation of cells with the virus inoculum was performed for 90 min. after which 8 ml. of Hink's medium with 10%FBS was added. After 3 days of incubation, cells were harvested and washed twice with PBS. Cells were lysed for 45 min on ice in twenty volumes of 1x insect cell lysis buffer (10 mM Tris pH 7.5, 130 mM NaCl, 1% Triton, 100 mM NaF, 10 mM NaPi, 10 mM NaPPI, with proteinase inhibitors: 16 mg/l benzamidine, 10 mg/l phenanthroline, 10 mg/l aprotinin, 10 mg/l leupeptin, 10 mg/l pepstatin A, 1 mM PMSF).

The lysate was cleared by centrifugation at 10.000 g for 30 min and the supernatant was batchwise incubated in TALON resin (with high affinity for the 6xHIS tag of the recombinant fusion protein). Binding was performed by gentle agitation for 20 min. at room temp. The resin was washed three times with lysis buffer, followed by an elution step with lysis buffer with 200 mM imidazole. Purified fusion protein was collected and purity and integrity was tested by SDS-PAGE.

#### Autophosphorylation assays

Protein kinase activity was determined by incubating 1 microgram of purified fusion protein for 30 min. at room temp. in a buffer containing 10 mM MgCl<sub>2</sub>, 10 mM MnCl<sub>2</sub>, 1 mM DTT and 10 μM [gamma-32]ATP (10<sup>5</sup> pm/pmol ATP). The autophosphorylated fusion protein was purified after SDS-PAGE from the gel in a buffer containing 50 mM NH<sub>4</sub>CO<sub>3</sub>, 0.1% SDS, 0.25% beta-mercaptoethanol. Protein was precipitated with 20 μg/ml BSA and 20% (w/v) solid trichloroacetic acid. The precipitate was collected after centrifugation, hydrolysed in 50 μl 6N HCl for 1 hour at 120 degrees Celcius. HCl was subsequently removed by lyophilization and the pellet was resuspended in a buffer consisting of 2.2% formic acid and 7.8% acetic acid. Hydrolysed protein was loaded onto cellulose thin layer chromatography plates together with control amino acid samples (phosphoserine, phosphothreonine, phosphotyrosine). Chromatography was performed in a buffer containing propionic acid: 1M ammonium hydroxide: isopropyl alcohol (90:35:35 v/v/v). After separation and drying of the plates, the separated amino-acids were visualized by spraying with 0.25% ninhydrin in aceton, followed by heating for 5 min. at 65 degrees Celcius. Plates were afterwards exposed to Phospho Imager cassettes in order to detect the phospho-labeled aminoacids.

#### SERK antibodies

Purified fusion proteins (10 μg) were mixed in complete Freund adjuvant and injected IP into BALBc mice. After 4 weeks booster antigen was injected (10 μg purified fusion protein in incomplete Freund adjuvant). Two weeks later a final booster was injected. One week after the final booster, serum was collected from these mice. The specificity and the titer of the resulting sera was tested on Western blots using total insect cell extracts with or without the SERK fusion proteins.

## INTRODUCTION OF THE SERK GENE INTO *PLANTA* AND THE PRODUCTION OF APOMICTIC SEED

### Carrot transformation with a SERK promoter fragment/luciferase gene fusion

The binary vector pMT500 is based on the pBIN19 vector (Bevan, 1984) and contains the firefly luciferase gene downstream of a polylinker containing 5 unique restriction sites was created by uni-directional ligation of the firefly luciferase coding region followed by the polyadenylation sequence from the pea *rbcS::E9* gene in the *Hind*III-*Xba*I site of the binary vector pMOG800 (kindly provided by Mogen N.V., Leiden, The Netherlands). The binary vector pMOG800 is based upon pBIN19 (Bevan, 1984) but while in pBIN19 the polylinker is flanked by the left border and the neomycin phosphotransferase (NPT II) expression cassette, the polylinker in pMOG800 is flanked by the right border and the NPT II expression cassette. From a genomic lambda clone, transcription regulating sequences from the carrot SERK gene were isolated by digestion with *Hind*III and *Dra*I (SEQ ID No. 1), and cloned into the *Hind*III / *Sma*I sites of pBluescript SK+. From the resulting vector a *Kpn*I / *Sst*I fragment containing the SERK genomic DNA was isolated and cloned into the *Kpn*I / *Sst*I sites of the binary vector pMT500. The resulting DNA construct, pMT531, contained the 2200 bp genomic SERK DNA fragment as promoter sequence, the luciferase gene as vital reporter, and the E9 transcription terminator sequence.

The binary vector pMT531 was transformed by electroporation into *Agrobacterium tumefaciens* strains MOG101 and MOG301 (for transformation into carrot cells) and into *Agrobacterium tumefaciens* strain C58C1 (for transformation into *Arabidopsis thaliana* plants). Transformed colonies were selected on LB plates with 100mg/l kanamycin.

### Transformation of carrot cells

The firefly luciferase coding sequence under control of the genomic carrot *Hind*III / *Dra*I 2200 bp DNA fragment was introduced into carrot cells by *Agrobacterium tumefaciens* mediated transformation of hypocotyl segments. Transformation of *Daucus carota* cv. 'Amsterdamse bak' was performed by slicing one week old dark grown seedlings into segments of 10 to 20 mm. Segments were incubated for 20 minutes in a freshly prepared 10 fold diluted overnight culture of *Agrobacterium*.. The segments were dried and transferred to a modified Gamborgs B5 medium (P1 medium; S&G seeds, Enkhuizen, The Netherlands) supplemented with 2 µM 2,4-D (P1-2) and solidified with agar (Difco, Detroit, Mi, USA ). After two days of culture in the dark at 25 ± 0.5 °C, segments were transferred to

solidified P1-2 medium supplemented with kanamycin ( $100 \text{ mg} \cdot \text{l}^{-1}$ ), carbenicillin ( $500 \text{ mg} \cdot \text{l}^{-1}$ ; Duchefa) and vancomycin ( $100 \text{ mg} \cdot \text{l}^{-1}$ ; Duchefa). After three weeks segments were transferred to fresh plates and transformed calli were selected after an additional three weeks. Transformed calli were grown on P1-2 plates with antibiotics for 3 weeks at a 16 hour light/8 hour darkness regime. Transformed embryogenic suspension cultures were initiated as described by transferring 0.2 g callus to 10 ml liquid P1-2 medium supplemented with  $200 \text{ mg} \cdot \text{l}^{-1}$  kanamycin,  $250 \text{ mg} \cdot \text{l}^{-1}$  carbenicillin and  $50 \text{ mg} \cdot \text{l}^{-1}$  vancomycin. During the first weeks 1 to 3 volumes of fresh medium were added to the culture at weekly intervals. After 5 to 7 weeks cultures were subcultured to a packed cell volume of 2 ml per 50 ml medium every two weeks and incubated at a 16 hour light / 8 hour darkness regime at  $25 \pm 0.5 \text{ }^{\circ}\text{C}$ .

One week after transfer to kanamycin selection medium, hypocotyl segments were sprayed with luciferin to test whether luciferase expression could be detected in transformed callus shortly after transformation. A large number of hypocotyl segments showed luciferase activity at the cut edges, but did not develop calli. Instead, growth of bacteria occurred, suggesting that the luciferase activity was of bacterial origin. Six to ten weeks after transformation, calli were obtained that showed luciferase activity in variable amounts, while no bacterial growth could be observed anymore. After 12 weeks, calli measuring 5 to 10 mm in diameter were used to start suspension cultures. At this time no bacterial contamination was observed. A control transformation experiment in which luciferase expression under influence of the CaMV 35S promoter was observed in single cells and cell clusters in the suspension culture demonstrating that the luciferase protein is active in *Daucus carota* suspension cultured cells.

#### Cell immobilisation

One-week old high-density ( $10^6$  -  $10^7 \text{ cells} \cdot \text{ml}^{-1}$ ) suspension cultures were sieved through nylon sieves with successive 300, 125, 50 and 30  $\mu\text{m}$  pore sizes (Monodur-PES; Verseidag Techfab, Walbeck, Germany). Single cells and cell clusters passing the last sieve are designated as  $< 30 \mu\text{m}$  populations. Control experiments with untransformed cells were performed with *Daucus carota* cv. 'Trophy' (S&G seeds) suspension cultures grown in P1-2 medium. Size fractionated cell populations smaller than 30  $\mu\text{m}$  were immobilised in phytigel (P8196; Sigma, St Louis, Mo, USA) in petriperm dishes (Heraeus, Hanau, Germany). The bottom layer consisted of 1 ml P1-0 medium with 5 mM  $\text{Ca}^{2+}$  and 0.2 % phytigel. Two

hundred thousand cells (< 30 µm and < 50 µm populations) in B5-0 medium without Ca<sup>2+</sup> supplemented with 0.1 % phytagel were poured on top of the bottom layer. For this layer B5 was applied since, at room temperature, phytagel solidified in P1 medium without Ca<sup>2+</sup>. After 2 hours of solidification an additional P1-0 layer with 0.2 % phytagel was poured onto the cell layer preventing the B5 layer to move. To prevent dehydration of the phytagel layers and to supply luciferin to the cells, 0.5 ml P1-0 medium containing 0.05 µM luciferin (Promega, Madison, Wi, USA) was added after solidification. The final luciferin concentration in the culture was 0.02 µM. Luciferin detection on single cells was determined with a CCD camera for a period of 5 times one hour (Schmidt et al. (1997) Development 124: 2049-2062). After 7 days of culture, luciferin was removed from the cultures by extensive washing with P1-0 medium.

#### Arabidopsis transformation with a SERK promoter fragment/luciferase gene fusion

Wildtype WS plants were grown under standard long day conditions: 16 hours light and 8 hours dark.

The first emerging inflorescence was removed in order to increase the number of inflorescences. Five days later, plants were ready for vacuum infiltration.

Agrobacterium strain C58C1 containing the transformation plasmid was grown on a LB plate with 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. A single colony was used to inoculate 500 ml of LB medium containing 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. The cultures were grown O/N at 28 degrees Celcius and the resulting log phase culture (OD600 0.8) was centrifuged to pellet the cells and resuspended in 150 ml of infiltration medium (0.5x MS medium (pH 5.7) with 5% sucrose and 10 µl/l benzylaminopurine). The inflorescences of 6 Arabidopsis plants are submerged in the infiltration suspension while the remaining parts of the plants (which are still potted) are placed upside down on meshed wire to avoid contact with the infiltration suspension.

Vacuum is applied to the whole set-up for 10 min. at 50 kPa. Plants are directly afterwards placed under standard long day conditions. After completed seed setting the seeds were surface sterilized by a 1% sodium hypochlorite soak, then thoroughly washed with sterile water and plated onto petridishes with 0.5xMS medium and 80 mg/l kanamycin in order to select for transformed seeds. After 5 days germination under long day conditions (10.000 lux), the transformed seedlings could be identified by their green color of their cotyledons

(the untransformed seedlings turn yellow), and were further grown in soil under C1 lab conditions under long day conditions. This vacuum infiltration method resulted in approximately 0.1% transformed seeds.

Transformation of a construct containing both a gene encoding kanamycin resistance and the 2200 bp (HindIII / DraI) SERK genomic DNA fused to the firefly luciferase gene into *Arabidopsis thaliana* (WS) by vacuum infiltration resulted in six different kanamycin-resistant primary transformants (I, II, III, IV, V and VI). Plants IV and VI died at the seedling stage, although they were kanamycin resistant. A T2 generation could be obtained from the four plants I, II, III and V (Figure 4). Within the siliques of the T2 generation of plants no. III and V, an early inhibition in development could be observed in approximately 25-50 % of the seeds. The plants I and II did not show a reduction in the number of developing seeds.(Figure 5). Similar results were observed in a T3 generation, in which again approximately 25-50% of the seeds showed an early inhibition of normal seed development.

#### Arabidopsis transformation with a AtSERK gene

##### Isolation of the AtSERK genomic and cDNA clones

Using the DcSERK cDNA sequence (seq ID no. 2) as a probe, a lambda ZipLox genomic library made from *Arabidopsis Landsberg erecta* total genomic DNA is screened for the presence of homologous sequences. Three different lambda clones with inserts of 14, 18 and 20 kb respectively are obtained. The 14 kb clone is digested by EcoRI and the resulting fragments subcloned into pBluescript vectors. Fragments spanning the entire coding sequence of the AtSERK gene are isolated, sequenced and compared with the *Daucus* homologues. The resulting sequence is shown as SEQ ID NO: 20.

Using the DcSERK cDNA sequence (SEQ ID NO: 2) as a probe, a lambda ZAPII cDNA library is screened for the presence of homologous sequences. Four lambda clones are obtained and their inserts subcloned into pBluescript vectors using the helper phage excision procedure. Fragments spanning the entire AtSERK cDNA coding sequence of the AtSERK gene are isolated, sequenced and compared with the *Daucus* homologues. The resulting sequence is shown as SEQ ID NO: 32.

#### Plasmids containing promoter sequences

*Arabidopsis thaliana* LTP1 promoter fragment is obtained from the binary plasmid pUH1000 (Thoma, S., Hecht, U., Kipper, A., Borella, J., De Vries, S.C., Sommerville, C. (1994) Plant Physiol. 105, 35-45) by digestion with *Bam*H1 and *Hind*III and cloning into pBluescript SK<sup>-</sup> (pMT121).

- The CaMV 35S promoter enhanced by duplication of the -343 to -90 region (Kay *et al.*, (1987) Science 236: 1299-1302) is isolated from the pMON999 vector by digestion with *Hind*III and *Sst*I and cloned into the pBluescript SK<sup>-</sup> vector (pMT120).

- The promoter AtDMC1 (Klimyuk and Jones (1997) Plant Journal 11: 1-14).

Plasmid SLJ 9691 is a construct consisting of pBluescript SK+ in which the *Arabidopsis thaliana* DMC1 genomic clone (accession number U76670) is cloned into the EcoRV site. SLJ 9691 carries EcoRV fragments of the 5' end of the AtDMC1 gene with the following modification: a *Bgl*II site instead of the second *Hpa*I site, two ATG codons in the first exon and an *Xba*I site at the ATG codon of the second exon.

- The FBP7 promoter from Petunia (Angenent *et al.* (1995) Plant Cell 7: 1569-1582).

The promoter of the FBP7 gene is cloned by subcloning the 0.6 kb *Hind*III - *Xba*I genomic DNA fragment of FBP7 into the *Hind*III - *Xba*I site of pBluescript KS-, resulting in the vector FBP201.

#### The pAtSERK binary vector constructs.

Based on the pBIN 19 vector, a binary vector pAtSERK is constructed for transformation of the *Arabidopsis thaliana* SERK cDNA under the control of different promoters.

The full length *Arabidopsis thaliana* cDNA clone of SERK (Seq ID No. NEW) is obtained from a pBluescript SK- plasmid. A *Sma*I - *Kpn*I 2.1 kb fragment containing the AtSERK cDNA is cloned into pBIN19 *Sma*I - *Kpn*I. The polyadenylation sequence from the pea *rbcS::E9* gene (Millar *et al.*, 1992), Plant Cell 4: 1075-1087) is placed downstream from the AtSERK cDNA by cloning a Klenow-filled *Eco*RI - *Hind*III E9 DNA fragment into the Klenow-filled *Xba*I site of the pBIN19:AtSERK vector in order to generate the binary vector pAtSERK.

#### Construction of plant expression vectors

The pAtSERK binary vector is used to generate the following promoter-AtSERK constructs.

- The AtLTP1 promoter is cloned in the SmaI site of the pAtSERK binary vector as a Klenow-filled *Kpn*I-*Sst*I DNA fragment to give the pAtLTP1AtSERK vector.
- The CaMV 35S promoter is cloned in the SmaI site of the pAtSERK binary vector as a Klenow-filled *Kpn*I-*Sst*I fragment to give the p35SAtSERK vector.
- The AtDMC1 promoter consisting of the *Bgl*II - *Xho*I 3.3kB fragment from the clone SLJ 9691 is filled in with Klenow and cloned into the SmaI site of the pAtSERK binary vector to give the pAtDMC1AtSERK vector.
- A *Sac*I-*Kpn*I fragment of FBP2101 is filled in with Klenow and cloned into the SmaI site of the pAtSERK binary vector to give the pFBP2101AtSERK vector.

#### Introduction of plant expression vectors into *Arabidopsis thaliana* plant cells

The above described vector constructs (pAtLTP1AtSERK, p35SAtSERK, pAtDMC1AtSERK, pFBP2101AtSERK) have been electrotransformed into *Agrobacterium tumefaciens* strain C58C1 as known in the art.

Wild type *Arabidopsis thaliana* WS plants are grown under standard long day conditions: 16 hours light and 8 hours dark.

The first emerging inflorescence is removed in order to increase the number of inflorescences. Five days later, plants are ready for vacuum infiltration.

*Agrobacterium* strain C58C1 containing the transformation plasmid (the pAtLTP1AtSERK vector or the p35SAtSERK or the pAtDMC1AtSERK vector or the pFBP2101AtSERK vector) is grown on a LB plate with 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. A single colony is used to inoculate 500 ml of LB medium containing 50 mg/l kanamycin, 50 mg/l rifampicin and 25 mg/l gentamycin. The cultures are grown O/N at 28 degrees Celsius and the resulting log phase culture (OD600 0.8) is centrifuged to pellet the cells and resuspended in 150 ml of infiltration medium (0.5x MS medium (pH 5.7) with 5% sucrose and 1 mg/l benzylaminopurine). The inflorescences of 6 *Arabidopsis* plants are submerged in the infiltration suspension while the remaining parts of the plants (which are still potted) are placed upside down on meshed wire to avoid contact with the infiltration suspension.

Vacuum is applied to the whole set-up for 10 min. at 50 kPa. Plants are directly afterwards placed under standard long day conditions. After completed seed setting the seeds are surface sterilized by a 1% sodium hypochlorite soak, then thoroughly rinsed with sterile water and plated onto petridishes with 0.5xMS medium and 80 mg/l kanamycin in order to select for transformed seeds. After 5 days germination under long day conditions (10.000 lux), the transformed seedlings could be identified by their green colour of their cotyledons (the untransformed seedlings turn yellow), and are further grown in soil under long day conditions. This vacuum infiltration method resulted in approximately 0.1% transformed seeds.

#### Expression of SERK sequences in *Arabidopsis thaliana* plant cells

The inflorescences from transgenic and not transgenic *Arabidopsis thaliana* plants are analysed by Whole mount *in situ* hybridisation analysis with AtSERK cDNA as probe. The inflorescences in different stages of development are fixed for 60 min. in PBS containing 70 mM EGTA, 4% paraformaldehyde, 0.25% glutaraldehyde, 0.1% Tween 20, and 10% DMSO. Samples are then washed, treated with proteinase K for 10 min, again washed and fixed a second time. Hybridisation solution consisted of PBS containing 0.1% Tween 20, 330 mM NaCl, 50 mg/ml heparin, and 50% deionized formamide. Hybridisation took place for 16 hours at 42°C using digoxigenin-labeled sense or antisense riboprobes (Boehringer Mannheim). After washing, the cells are treated with RNaseA and incubated with anti-digoxigenin-alkaline phosphatase conjugate (Boehringer Mannheim) which had been preabsorbed with a plant protein extract. Excess antibody is removed by washing followed by rinsing in staining buffer (100 mM Tris-HCl pH 9.5, 100 mM NaCl, 5 mM MgCl<sub>2</sub>, 1 mM levamisole) and the staining reaction is performed for 16 hours in a buffer containing NBT and BCIP. Observations are performed using a Nikon Optiphot microscope equipped with Nomarski optics.

The transformed plants show ectopic expression of SERK in the vicinity of the embryo sac.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: NOVARTIS AG
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- (I) TELEX: 962 991

(ii) TITLE OF INVENTION: Improvements in or relating to organic compounds

(iii) NUMBER OF SEQUENCES: 33

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Daucus carota

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3696..6617

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 3731..3802

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 3851..3979

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4124..4211

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4284..4357

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4430..4528

(ix) FEATURE:

(A) NAME/KEY: intron

(B) LOCATION: 4642..4757

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 4890..4967

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 5295..5803

(ix) FEATURE:

- (A) NAME/KEY: intron
- (B) LOCATION: 6197..6339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCTAGATGAC GAAATCGCGC TACCTTTGAT TTGAAATAC TAGTTTGTAG TATCTTGATT	60
AGTTTTTTGG ATATCTTGCT GAAATTTCCT TAGGAGATGC AAACGGTCTT CATTAAATAT	120
GAGCCCTTGT GACTTGACAA AAGTATCTAG CATTTTGAT CACGAGGTAG CTAAAAAGTA	180
GCGTGTGTTGA TTAAGCACAT AATATTGTAT TGGGCCTATT GGCTATCAAT GAAGTTTGAT	240
GCAAGTATAT AGCTTGTATT ATGCATGTGA TGAGGGTATA TAAAAGAAGT AAAGAACATT	300
CTCTCGTAGC ATTCACTTTT CTCTTGCCTA TAGTTAACGA GTTTTGTAC ACATGACGTT	360
GAAACTGGAT GTGTCGTTC TTCCATCTAA GTTGGATTA CCTGATAGAT GCTCAACTTC	420
TTCGTCAGCC TTTCTTTCC GATTTCCTCC AAGACAAGAT TCCTTAGTTA ATAGTTATTG	480
CTCTGGTGGC TTGTCGTGCAT TTTAGGAATC TTACTCTGTT TTTTAATGGA GAAACGAAAC	540
CTACCTTTTT TTCTGTGTTT CCTTTTATGA TATCACCTGC TTGGAGGCCT TTAGACTTTA	600
TCCACCTAAA CTATTCATGT TTACCAGACA AGCTATACGT TTTATCCCCC CCCCCCGCGG	660
ACCTGNGGAC AAAAGAAGCG CTGATGAAT GATTAAATCC GTGTTTATT ATATTACACA	720

TTGATGCCTC ATGGAGCTAA TATCTTGGT TAAATTTCAT GTATATATAT ACCCTCCCT 780  
CTTGTGATGG CAGTGGCCCC TCGTTTAATT AGCGTACTTA ATTATCTGAT GGATACTGTA 840  
TGCTTGGCAG ATGATGTCAT CAGATTATAC CATTGTTGT GCTCTACAAA ATAAAAAACC 900  
TCTATTTATG TTCATCTTT TGGTAACAAG TAACTAATTG ATGCGCTATG TTGACAGGCG 960  
ATGCATTACA CAACTTACGA ACTAGCTTGC AAGATCCAA CAATGTCCIG CAGAGCTGGG 1020  
ATCCAACCT TGTGAACCT TGCACATGGT TTCATGTGAC ATGTAACAAT GAAAACAGTG 1080  
TTATAAGAGT GTAGGTCACT TCCCTTATTA ATTTTTTAG CAAGTTACGA ATATTACTC 1140  
AATTGAGCAG ATGTCCTTT AAATATTTC CTTTAATTTC TTAGCTAACG GGAGCATCTA 1200  
TCTTAAGTAT CTCTACTGAA TTAAAGACAT AATACATTTC TTAAAAAAAT CTATTAGAGT 1260  
GTTTTTCG CACAGOGCAC ATATATCTT TTCTGGTAA TTCAGACAAAC CTTTCTCCCG 1320  
ACGATAAAAT AATATAAGAT TAACTCCITG AACTAATTTC TTATTTCTT TTCTTTTA 1380  
TGTCTTTGC AGAAAGTTTC TTATGGCTT TTGTGAAAAG TACATTCTAT GATAATTTT 1440  
TGGCAACTCA TATAAATTTC TATATATTCC ATGTAGTTAT AAGTTAAAAA AAGCTTCCTA 1500  
TTAATTCCAA GATAGAGGTT CATTTTATAA GTTGGGCAT CCATGAGTT TTGAAAATGT 1560  
CAGAAATTTC TTGAGTTAA TTTTACTTAC CAACTTTAT GGCCTCATGC AGTGAATCTG 1620  
GGAATGCAGC ATTATCTGGT CAATTGGTTC CTCTGGCCA GTGAAAAAT TTACAATACT 1680  
TGTAAAGACCA TATCACTTGG AATGCTTGT TTTTATACA GCACAATGCT TTCAATATCT 1740  
GTTAAAAGTG TGAAAAGTT GACTTTCTAG CTTCAAGCACT TGTTGGATA ATATCTATGA 1800

AGCACCTAAA AGGCTGGCA ATTTTTTGT TATTATTC AATATTGTTA ATTGTTACTA 1860  
CTTAATATGA TAAACTGATT TAACCTCTCA TGATGGTCT CAGTCCAATG TGCCCTCATT 1920  
AGTCACATNA TAAAATTGGN GGGTTGGACA AATATAACIT CTTTCTTAA GGTCCAGAAA 1980  
GAGCACTTAT CAACCTTGTC TAGCGCATAA CGTCACAGTG GGTCAGTCAC GGGCTATCCA 2040  
GTTTGGGAG GTTTAATGA GCACCTTATT ACCTTGTCTT TTAAACGTCT GAGGATGTTA 2100  
TTAAAGCTG CATCATTCAG AGTTTAAATT AGCACCTICA GTGTTATTAT GAATGGTACA 2160  
TGAAAGATAC ATATCTTAAT GTTCCTATGC CTGTTCAAC ATGTCCTAA TATTCTGTTA 2220  
TCTTGTCTAT CTTAAAATG GCACGTGATTA AAATGTGAGA AAGGTAGTCT TCCAATACCA 2280  
TTTCATGTAT ACCAGAGAAT ATCATAATT TTTAAATCA TAAGTTGGC CCTAGAGTTT 2340  
TCTCAGTATT GGTCTATTAA TATTTCCAC CATTAGAAC TGTGTTGTCA GATGAAAATC 2400  
TTGGACTTCC ACAGAAGATC TTATAGTAAA AGTATTCTTT AGATCTGATG ATGAAAGTTG 2460  
TCATGGTGTG GCTGTGCCA GAATTAAAT CAATCCCATG TCACATGTTT GTGATCTGA 2520  
CTACTCACTG TTAATCGAAG AGTAACATT TGTGAATTAA ATGCTTTTTT TTTTGTCTT 2580  
CATGCTTAGC GTTATAAAGG TCTACGTCTG ACTATGGTTT TTAACATGTT ATAGTTTGT 2640  
ACTGACAAGT TTAAAGTTTC TCTTGTCTAC GAATTAAGAA TATATAATAT AAAACGCTTT 2700  
AACTTTCTCT GTGGAAGGTG TTCTTACCTT TTTATATATA TATATAGATA CTCAGACTCT 2760  
GCTGGCAATT ATATCTTACG AACCTACGAG TATACAGAAC TTGTATATTA GGTCAGATG 2820  
AGTGGCTGTA GTAGAACACC TTAAGCAAGA ACTTAATCAT GAGGTTCAA CCTTTTAAC 2880  
TTCTTTTAG ATTTTTCAA GTTATGGAA AATTGTACCT CATGATCGTG GTTCTTTCC 2940

ATAAAACTTTC CATATAAGTC CGTTTCTTGA CGTTTCATG TAAGCTGTG ACGAGTGATT 3000  
ATTAGCGGGTT CTTCAATAA TCATAATGTG TCTCAGTTTG ATGAGGCCTG TACTTATTAT 3060  
TGCACCTTGC ACTTAACCTT GATCCTCATG TCATCTTGTAT TGTCATAGTC TACTAACCGA 3120  
GTTGAACATG GTTTATCATG TCTTTGAGG TAACAATGTA GCTTTCACCT CTGTCCTTGA 3180  
TATAGGTTTA AGGCTTGCAC CTCCCCACTAG CCTTTGGTTG TTTTATTACAC AGTTCACACA 3240  
CCTACTAGCA CTGTTCACCT CTAGTCCTTT GTCCGCAAAT AGTAAGAAGT TTCTTCGCA 3300  
TAATAGTGGGA TGATCATTAA AGAAATAGTG AATCAAATTAA TCGTGTATT GTGTTGTAC 3360  
TTTGGAAATTA AATGAGITGC TGAACATTTG TGCTGTATTAT CGTTGTCAAG GCTTTGCCAA 3420  
GGAAGGCGAT TAGTAAGAGT GGGCATCCAA GCGCCCTTAT CTTGAAGGGG CGGGCGGCAC 3480  
GTTGIGGATT CTGGGTGTCT ATTAGAGGAC ATTATCTATA TATACTGATT ATTTATTAGA 3540  
ATATAAAATCA ACTACTATAT TTTCTTTGT AATGTTTATA TAGAAATCCC ACTCGTAAAC 3600  
TTGACAAATA CCATTGAAAT ATTGAAACCT AATTAATTAG TAGTGTCAAGG TTTAAATTCA 3660  
AACTCATTTA ATTTTACTTT AAAAAATAAT TCTATATGAA TCGTAACAGT ATAAATATAT 3720  
TAAATTACAT GTATGIGTGC CTATATATAG CTGAATGTCT AATAGACTCC AAGACGGCTG 3780  
CTCTTACTGC CTAGGCGTCC AGGCAGTTCA CTGATGCTTA CCTTGACAAA TATGGGGTTC 3840  
GTATGACATT GTGGGGATC CCTATCACTG GATTCTGTT TTGCTGACCC TCTGTTCAAT 3900  
TGATTTCAT TGATGTAGTA TTACTAGTTT TATAATATT CTTTATTGCA ATAATTTAAC 3960  
TGGAGTTTAA CAATGACAGG GAGCTTTACA GCAATAACAT AAGTGGACCA ATTCTAGTG 4020

ATCTTGGGAA TCTGACAAAT TTGGTGAGCT TGGACCTATA CATGAATAGC TTCTCTGGAC 4080  
CTATACCGGA CACATTAGGA AAGCTTACAA GGCTAAGATT CTGTATGAC TACAAATCIT 4140  
CACTAGTTT TAACTTAATG CAATTGATT ATCCCTCAA GTGATTGATT ATATCACAAA 4200  
TTACTGGATA GGCGTCTCAA CAACAACCTGC CTCTCTGGTC CAATTCCAAT GTCACIGACT 4260  
AATATTACAA CTCTTCAAGT CCTGTAAGTA TTCCGACCTT TCCAGATAGT TTGTTGTTG 4320  
TGGATGTTTC AATTAAATA CTAAATATGT TCATCAGGGA TTATCAAAC AATCGGCTAT 4380  
CAGGACCAGT ACCGGATAAT GGCTCATTTT CTMGTTCAC ACCTATCAGG TTTAATGCTA 4440  
GTAATATCIT TAATATTATG GTCTTACTT CTACTGCGAA AGCTATGATA ATATTTTTT 4500  
TCTCCCTCAT ATATTATCAC TTTCGCAGTT TTGGCAATAA TTGAATTAA TGTTGACCTG 4560  
TAACTGGGAG GCCCTGCCCT GGATCTCCCC CATTCTCTCC ACCACCTCCG TTCACTCCCAC 4620  
CATCAACAGT ACAGCCTCCA GGTGATTTAG TTTTATATT AATTCCCGTA ATTAAATTITA 4680  
TGACTGTAAA AATTGGTGT AATTTCACCA GTTGCAGATA AAGTATTTTC CTCTTTCTC 4740  
TTCTTATTAT TATGAAGGAC AAAATGGTCC CACTGGAGCT ATTGCTGGGG GAGTAGCTGC 4800  
TGGTGCTGCT TTACTGTTTG CTGCACCTGC AATGGCATT GCATGGTGGC GGAGAAGAAA 4860  
ACCGCGAGAA CATTCTTTG ATGTGCCAGG TTAGTCCGT AAATAGATAT CTATTGAAGC 4920  
GCTTACTGTC TGIGGACTTT GTTTTCACTG TCATTAGTTA ACTTCAGCTG AAGAGGACCC 4980  
AGAAGTGCAC CTGGTCAAC TGAAGAGGTT TICCTGCGA GAATTGCAAG TCGAACCGGA 5040  
TACTTTAGT ACCATCCTTG GAAGAGGTGG AATTGGTAAG GTGTATAAGG GACCCCTTGC 5100  
TGATGGCTCA CTGTAGCAG TTAAAAGGCT TAAAGAAGAA CGAACACCAAG GTGGCGAGCT 5160

GCAGTTCAA ACAGAAGTGG AAATGATTAG CATGGCTGTG CATGAAATC TTCTGGTCT 5220  
ACGTGGTTTC TGCATGACAC CTACCGAGCG GCTTCCTGTA TATCCATACA TGGCTAATGG 5280  
AAGTGTTGCG TCAATGTTAA GAGGTATCTC AGTTACAAIT ACCATAACIT GCCAGAAGTT 5340  
TGTTTGATTA AAAATGAAAT ATAACCTCCCT ACACATATGTT AAGGTGTTAT AATTTCTGAG 5400  
CAGATCTTAT TTCCCATTCGC AAGATACCAG TTATTATTGT TTTTCTGTA ATTGATACCG 5460  
GTTATATTTC TTCTTGTAT TTGGTTATAT GCAAGGATTT CGAGTCTAAT AAGTTATCAA 5520  
ACTGGATGCT ATGTTTATTC TGCAATTGAA TTCTTGCTTC ATGTGCCAAA ATATATATGA 5580  
TTCAACTTGG AATCATCTTA TAATATACIG TGTAAGTCAG GCTGTTGACT TTCTATCTTA 5640  
ATTAGTCCTC ATAAATCAGA ATCTGCCTAG TGAGCTTTAC CGACATACTC TAAACCTTTC 5700  
TTATGGCCCT GTATATAATC GTCACCTTA CTTTATTCAAG TTGTCTGCT CTCTGAATTT 5760  
TTGATCTGTA CATTGTGATG TCTTGTCTTC ATCAAATGTA GAGCGTCAGC CATCAGAAC 5820  
TCCCCCTGAT TGGCCAACTA GGGAGAGGAT TGCACTAGGA TCTTCTAGGG GCCTATCTAA 5880  
ATTGCATGAC CATTGTGATC CCAAGATTAT CCATCGCGAT GTAAAAGCTG CAAATATATT 5940  
ATTGGACGAA GAATTGAGG CTTGTGAGG TGATTTGGG TTAGCTAGGC TCATGGATTA 6000  
CAAGGATAACC CATGTTACGA CTGCTGTAAAG GGGTACCAATT GGGCACATAG CTCCCCAGTA 6060  
CCTCTCGACT GGAAAGTCAT CAGAGAAGAC CGATGCTTT GGTTATGGGA TAATGCTCT 6120  
AGAGCTCATT ACTGGACAGA GGGCTTTGTA TCTTGCTCGC CTGGCGAACG ATGATGATGT 6180  
TATGTTGTG GATTGGGTAT GTGTCCCGGG TGTTCCCTTG GTTAATTATT TCACATATTA 6240

GIGCTTACTA CTTTGTGTCG GCCCTTTGTT TTTATTCCT GCCGTGATTG GATTCTTAGT	6300
CATGTTATGC ATATTGACCT GCTTTGCAAT GTCCTTTAGG TTAAAAGCCT TTTGAAAGAG	6360
AAAAAGTTGG AGATGCTGGT CGATCCGTAC CTGCAGAACCA ATTACATTGA CACAGAAGTT	6420
GAGCAGCTTA TTCAAGTAGC ATTACTCTGT ACCCAGGGTT CGCCAATGGA GCGGCCTAAG	6480
ATGTCAGAGG TAGTCCGAAT GCTTGAAGGT GATGGCCTTG CAGAAAAGTG GGACGAGTGG	6540
CAAAAAGTTG AAGTCATCCA TCAAGACGTA GAATTAGCTC CACATCGAAC TTCTGAATGG	6600
ATCCTAGACT CGACAGATAA CTTGCATGCT TTTGAATTAT CTGGTCCAAG ATAAACAGCA	6660
TATAAAATGT AATGAAATTA ATATTTTTA TGGTT	6695

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Daucus carota

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 94..1752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GACAAATACC ATTGAAATAT TTGAACCTAA TTAATTAGTA GTGTCAGGGT TAAATTCAAA	60
CTCATTAAAT TTTACTTTAA AAAATAATTIC TAT ATG AAT CGT AAC AGT ATA AAT	114
Met Asn Arg Asn Ser Ile Asn	
1 5	
ATA TTA AAT TAC ATG CAG TTC ACT GAT GCT TAC CTT GAC AAA TAT GGG	162
Ile Leu Asn Tyr Met Gln Phe Thr Asp Ala Tyr Leu Asp Lys Tyr Gly	
10 15 20	
GTT CTT ATG ACA TTG GAG CTT TAC AGC AAT AAC ATA AGT GGA CCA ATT	210
Val Leu Met Thr Leu Glu Leu Tyr Ser Asn Asn Ile Ser Gly Pro Ile	
25 30 35	
CCT AGT GAT CTT GGG AAT CTG ACA AAT TTG GTG AGC TTG GAC CTA TAC	258
Pro Ser Asp Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr	
40 45 50 55	
ATG AAT AGC TTC TCT GGA CCT ATA CCG GAC ACA TTA GGA AAG CTT ACA	306
Met Asn Ser Phe Ser Gly Pro Ile Pro Asp Thr Leu Gly Lys Leu Thr	
60 65 70	
AGG CTA AGA TTC TTG CGT CTC AAC AAC AAC AGC CTC TCT GGT CCA ATT	354
Arg Leu Arg Phe Leu Arg Leu Asn Asn Asn Ser Leu Ser Gly Pro Ile	
75 80 85	
CCA ATG TCA CTG ACT AAT ATT ACA ACT CTT CAA GTC CTG GAT TTA TCA	402
Pro Met Ser Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser	
90 95 100	
AAC AAT CGG CTA TCA GGA CCA GTA CCG GAT AAT GGC TCA TTT TCT TTG	450
Asn Asn Arg Leu Ser Gly Pro Val Pro Asp Asn Gly Ser Phe Ser Leu	
105 110 115	
TTT ACA CCT ATC AGT TTT GCC AAT AAT TTG AAT TTA TGT GGA CCC GTA	498

Phe Thr Pro Ile Ser Phe Ala Asn Asn Leu Asn Leu Cys Gly Pro Val  
120 125 130 135  
  
ACT GGG AGG CCC TGC CCT GGA TCT CCC CCA TTT TCG CCA CCA CCT CGG 546  
Thr Gly Arg Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Pro  
140 145 150  
  
TTC ATC CCA CCA TCA ACA GTA CAG CCT CCA GGA CAA AAT GGT CCC ACT 594  
Phe Ile Pro Pro Ser Thr Val Gln Pro Pro Gly Gln Asn Gly Pro Thr  
155 160 165  
  
GGA GCT ATT GCT GGG GGA GTA GCT GGT GCT GCT TTA CTG TTT GCT 642  
Gly Ala Ile Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Leu Phe Ala  
170 175 180  
  
GCA CCT GCA ATG GCA TTT GCA TGG TGG CGG AGA AGA AAA CCG CGA GAA 690  
Ala Pro Ala Met Ala Phe Ala Trp Trp Arg Arg Lys Pro Arg Glu  
185 190 195  
  
CAT TTC TTT GAT GTG CCA GCT GAA GAG GAC CCA GAA GTG CAC CTT GGT 738  
His Phe Phe Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly  
200 205 210 215  
  
CAA CTG AAG AGG TTT TCT CTG CGA GAA TTG CAA GTC GCA ACG GAT ACT 786  
Gln Leu Lys Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Thr Asp Thr  
220 225 230  
  
TTT AGT ACC ATA CTT GGA AGA GGT GGA TTT GGT AAG GTG TAT AAG GGA 834  
Phe Ser Thr Ile Leu Gly Arg Gly Phe Gly Lys Val Tyr Lys Gly  
235 240 245  
  
CGC CTT GCT GAT GGC TCA CTT GTA GCA GTT AAA AGG CTT AAA GAA GAA 882  
Arg Leu Ala Asp Gly Ser Leu Val Ala Val Lys Arg Leu Lys Glu Glu  
250 255 260  
  
CGA ACA CCA GGT GGT GAG CTG CAG TTT CAA ACA GAG GTG GAA ATG ATT 930  
Arg Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile

265	270	275	
AGC ATG GCT GTG CAT CGA AAT CTT CTG CGT CTA CGT GGT TTC TGC ATG           978			
Ser Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met			
280	285	290	295
ACA CCA ACA GAG CGG CTT CTT GTA TAT CCA TAC ATG GCT AAT GGA AGT           1026			
Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser			
300	305	310	
GTT GCG TCG TGT TTA AGA GAG CGT CAG CCA TCA GAA CCT CCC CTT GAT           1074			
Val Ala Ser Cys Leu Arg Glu Arg Gln Pro Ser Glu Pro Pro Leu Asp			
315	320	325	
TGG CCA ACT AGG AAG AGG ATT GCA CTA GGA TCT GCT AGG GGG CTT TCT           1122			
Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser			
330	335	340	
TAT TTG CAT GAC CAT TGT GAT CCC AAG ATT ATC CAT CGT GAT GTA AAA           1170			
Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys			
345	350	355	
GCT GCA AAT ATA TTA TTG GAC GAA GAA TTT GAG GCT GTT GTA GGT GAT           1218			
Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp			
360	365	370	375
TTT GGG TTA GCT AGG CTC ATG GAT TAC AAG GAT ACC CAT GTT ACA ACT           1266			
Phe Gly Leu Ala Arg Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr			
380	385	390	
GCT GTA AGG GGT ACC TTG GGC TAC ATA GCT CCC GAG TAC CTC TCG ACT           1314			
Ala Val Arg Gly Thr Leu Gly Tyr Ile Ala Pro Glu Tyr Leu Ser Thr			
395	400	405	
GGA AAG TCA TCA GAG AAG ACC GAT GTC TTT GGT TAT GGG ATT ATG CTC           1362			
Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu			
410	415	420	

TTA GAG CTC ATT ACT GGA CAG AGA GCT TTT GAT CTT GCT CGC CTT GCG 1410  
Leu Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala Arg Leu Ala  
425 430 435

AAC GAT GAT GAT GTT ATG TTG TTG GAT TGG GTT AAA AGC CTT TTG AAA 1458  
Asn Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Ser Leu Leu Lys  
440 445 450 455

GAG AAA AAG TTG GAG ATG CTG GTC GAT CCT GAC CTG GAG AAC AAT TAC 1506  
Glu Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Glu Asn Asn Tyr  
460 465 470

ATT GAC ACA GAA GTT GAG CAG CTT ATT CAA GTA GCA TTA CTC TGT ACC 1554  
Ile Asp Thr Glu Val Glu Gln Leu Ile Gln Val Ala Leu Leu Cys Thr  
475 480 485

CAG GGT TCG CCA ATG GAG CGG CCT AAG ATG TCA GAG GTA GTC CGA ATG 1602  
Gln Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val Val Arg Met  
490 495 500

CTT GAA GGT GAT GGC CTT GCA GAA AAG TGG GAC GAG TGG CAA AAA GTA 1650  
Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp Gln Lys Val  
505 510 515

GAA GTC ATC CAT CAA GAC GTA GAA TTA GCT CCA CAT CGA ACT TCT GAA 1698  
Glu Val Ile His Gln Asp Val Glu Leu Ala Pro His Arg Thr Ser Glu  
520 525 530 535

TGG ATC CTA GAC TCG ACA GAT AAC TTG CAT GCT TTT GAA TTA TCT GGT 1746  
Trp Ile Leu Asp Ser Thr Asp Asn Leu His Ala Phe Glu Leu Ser Gly  
540 545 550

CCA AGA TAAACAGCAT ATAAAATGTG AATGAAATTA ATATTTTTA TGGTTAAAAA 1802  
Pro Arg

AAAAAAAAAA AAA

1815

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Asn Arg Asn Ser Ile Asn Ile Leu Asn Tyr Met Gln Phe Thr Asp  
1 5 10 15

Ala Tyr Leu Asp Lys Tyr Gly Val Leu Met Thr Leu Glu Leu Tyr Ser  
20 25 30

Asn Asn Ile Ser Gly Pro Ile Pro Ser Asp Leu Gly Asn Leu Thr Asn  
35 40 45

Leu Val Ser Leu Asp Leu Tyr Met Asn Ser Phe Ser Gly Pro Ile Pro  
50 55 60

Asp Thr Leu Gly Lys Leu Thr Arg Leu Arg Phe Leu Arg Leu Asn Asn  
65 70 75 80

Asn Ser Leu Ser Gly Pro Ile Pro Met Ser Leu Thr Asn Ile Thr Thr  
85 90 95

Leu Gln Val Leu Asp Leu Ser Asn Asn Arg Leu Ser Gly Pro Val Pro  
100 105 110

Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro Ile Ser Phe Ala Asn Asn  
115 120 125

Leu Asn Leu Cys Gly Pro Val Thr Gly Arg Pro Cys Pro Gly Ser Pro  
130 135 140

Pro Phe Ser Pro Pro Pro Phe Ile Pro Pro Ser Thr Val Gln Pro  
145 150 155 160

Pro Gly Gln Asn Gly Pro Thr Gly Ala Ile Ala Gly Gly Val Ala Ala  
165 170 175

Gly Ala Ala Leu Leu Phe Ala Ala Pro Ala Met Ala Phe Ala Trp Trp  
180 185 190

Arg Arg Arg Lys Pro Arg Glu His Phe Phe Asp Val Pro Ala Glu Glu  
195 200 205

Asp Pro Glu Val His Leu Gly Gln Leu Lys Arg Phe Ser Leu Arg Glu  
210 215 220

Leu Gln Val Ala Thr Asp Thr Phe Ser Thr Ile Leu Gly Arg Gly Gly  
225 230 235 240

Phe Gly Lys Val Tyr Lys Gly Arg Leu Ala Asp Gly Ser Leu Val Ala  
245 250 255

Val Lys Arg Leu Lys Glu Glu Arg Thr Pro Gly Gly Glu Leu Gln Phe  
260 265 270

Gln Thr Glu Val Glu Met Ile Ser Met Ala Val His Arg Asn Leu Leu  
275 280 285

Arg Leu Arg Gly Phe Cys Met Thr Pro Thr Glu Arg Leu Leu Val Tyr  
290 295 300

Pro Tyr Met Ala Asn Gly Ser Val Ala Ser Cys Leu Arg Glu Arg Gln  
305 310 315 320

Pro Ser Glu Pro Pro Leu Asp Trp Pro Thr Arg Lys Arg Ile Ala Leu

325

330

335

Gly Ser Ala Arg Gly Leu Ser Tyr Leu His Asp His Cys Asp Pro Lys  
340 345 350

Ile Ile His Arg Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Glu Glu  
355 360 365

Phe Glu Ala Val Val Gly Asp Phe Gly Leu Ala Arg Leu Met Asp Tyr  
370 375 380

Lys Asp Thr His Val Thr Thr Ala Val Arg Gly Thr Leu Gly Tyr Ile  
385 390 395 400

Ala Pro Glu Tyr Leu Ser Thr Gly Lys Ser Ser Glu Lys Thr Asp Val  
405 410 415

Phe Gly Tyr Gly Ile Met Leu Leu Glu Leu Ile Thr Gly Gln Arg Ala  
420 425 430

Phe Asp Leu Ala Arg Leu Ala Asn Asp Asp Asp Val Met Leu Leu Asp  
435 440 445

Trp Val Lys Ser Leu Leu Lys Glu Lys Lys Leu Glu Met Leu Val Asp  
450 455 460

Pro Asp Leu Glu Asn Asn Tyr Ile Asp Thr Glu Val Glu Gln Leu Ile  
465 470 475 480

Gln Val Ala Leu Leu Cys Thr Gln Gly Ser Pro Met Glu Arg Pro Lys  
485 490 495

Met Ser Glu Val Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys  
500 505 510

Trp Asp Glu Trp Gln Lys Val Glu Val Ile His Gln Asp Val Glu Leu  
515 520 525

Ala Pro His Arg Thr Ser Glu Trp Ile Leu Asp Ser Thr Asp Asn Leu  
530                    535                    540

His Ala Phe Glu Leu Ser Gly Pro Arg  
545                    550

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTTTTTTTT TGC

13

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGGATCTAAG

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

ACACGTGGTC

10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCAGCACAGG

10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TTTTTTTTTT TCTG

14

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTTTTTTT TCA

13

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GACATCGTCC

10

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCCTACTGGT

10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

ACACGTGGTC

10

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGTGACTGTC

10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TCTTGGACCA GATAATT

18

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCTGATGAC TTTCCAGTC

19

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AATGGCATTT GCATGG

16

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Daucus carota

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ser Pro Pro Pro Pro  
1 5

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Daucus carota

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

His Arg Asp Val Lys Ala Ala Asn

1

5

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Daucus carota

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Gly Thr Leu Gly Tyr Ile Ala Pro Glu

1

5

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: *Arabidopsis SERK gene*

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1280..1367

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1796..1928

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2014..2085

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2203..2346

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2450..2521

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2617..2688

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2772..2884

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 3015..3146

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 3305..3646

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 3760..4081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTAGAAACC TTTTGATCAT AATGAAAATA AAGAGTCCAT CCACCACATG GGGTAAGCAT	60
AATGTGTGAT ATTTAAAGGG TAACAAATGT AATCTGCITT TTATTTACT TTTTACCTCT	120
ACTCAAATIG TATGGGCAGT TTTTTTTTTT TTTAAATGA TAAGACAAGT ATCTGTTAA	180
TGGTATTGTG ATGAAACAGT AGTAAAGTCA TATCGGGCAC GCCATACTAC TTCCACAGTG	240
GAACITGGCC AAATTTTGTG TTTGCGTCT CTACAGTTTC TTCCACCAAA TTTTTTGTG	300
ACAAAACCTCA AATCTTCAA TCTCATCTCT GCCAAAGTTG GGTTTAGAAA GAATATCAGC	360
AAACACTAAT ATCTTTATTG TTGCATGGTT TATCAATCAC AAAATTACACA ACCATTGTAA	420
AAAAAAATTC ACATTTTGG TATGAGATIG CTCACATGAT AGTGAACCTC TTTAACATTT	480
TAACTTTACT TTCATAAATA CGGGATTACG AATCTTACTTT GCATTAAGAAA TTTAGAAAAG	540
GTTTTCTAC TTAAAGAAAA AAGGGACCCA ACAGAGAGAG GTTTGACCAAG GAGAACGGG	600
TGCATAGCCT TAAGAGCTTT CAACTACTTT ACCCCAAACC CAAAGCGATG TCACTTCAA	660
CCATCTCTTC TCTCCCCCGA ACCCGTTTTT TTGACCGGTC AGTTGGGCA GCAGCACCGT	720
TACGGGCAGC TTATATTCT CGTCCTCTC CTCTACACCA CTGCATGCCA ATAATAAAG	780

CCCGTTGAGA TCTTAAAAAA TATTAATAA TATATCAACG AAAAAGCTAT TTATTCATA 840  
AGAAGAAAAA GAGAGGAACA ACAACAACAC ACTAATCATA GTTCTCTGG CAGGCTGTT 900  
GTGCGGCCTT AATAAAAAGC TCTTTGTTA TTATTACTTC ACAGTAGATTT TCCCCAAAAA 960  
GCTCTTATTT TTTGTTAA AAAAAAAAGT TTCATCTTAA TICAACCTTT GTTTACAGT 1020  
GTGTGTGTA GAGAGAGAGT GTGGTTTGAT TGAGGAAAGA CGACGACGAG AACGCOGGAG 1080  
AATTAGGATT TTATTTTAT TTTTACTCT TGTGTTGTT TAATGCTAAT GGGTTTTAA 1140  
AAGGGTTATC GAAAAATGA GTGAGTTGT GTTGAGGTG TCTCTGAAA GTGTTAATGG 1200  
TGGTGATTT CGGAAGTTAG GGTTTCTCG GATCTGAAGA GATCAAATCA AGATTCGAAA 1260  
TTTACCATG TTGTTGAAA TGGAGTOGAG TTATGTGGTG TTATCTTAC TTTCACTGAT 1320  
CTTACCTCCG AATCATTACAC TGTGGCTTGC TTCTGCTAAT TTGGAAGGTT CGTGGTTACT 1380  
CAATTACTCA GCTTACTCG TTCTCAATT ACCTTCTCGA TTCTTTTTA TTGGAGGTG 1440  
AATCGCTATC TTAGTGTCT GCATTTGAT TTATGAAAAT TGTGTTGTT CTGTTATTT 1500  
GTAAGATTAA GTGGCTAGTA CTTGAATAC ACTGTTTGC TTTCTTGT CAGATCACT 1560  
TTGTATATTG TAAAGGCATG TTCTTGGGT TGAAAAGCTG GGTTATTTGA TATCTTAAGA 1620  
TTGATGTTGT TGATCCAAAC ATTCCTCGAA AGACTCTAAT TTGTTTGTGTT TTGTTAAAGA 1680  
ATTTGTTAA TTATTAGCCT CTAATCTCAG AGAGGCCGTG TTGAATAGIT CTCTCTGAA 1740  
ATTAGACTTT TCACCAATTG ATGCTAATTG TGTAGATTIG TTGTTCTTGT TATAGGTGAT 1800  
GCTTGCATA CTTGAGGGT TACTCTAGTT GATCAAACA ATGCTTGCAG GAGCTGGGAT 1860  
CCTACGCTAG TGAATCCCTG CACATGGTTC CATGTCACCTT GCAACAAACGA GAACAGTGTC 1920

ATAAGAGTGT AAAGCTTCT TCTACTAATC CCACTTTTA AACTTTGACC TCAGCGTGGT 1980  
TACCGACATT TTGTTTCCTT TTGTCAAATA CAGTGATTTG GGGATGCAG AGTTATCTGG 2040  
CCATTTAGTT CCAGAGCTTG GTGTGCTCAA GAATTGGCAG TATTIGTAAG TTCCACCTAT 2100  
GCATCATGCT TTAACAAAAC AAATCCAAGA TTGACAGAA GAAGCACTGG AGTTACCTTT 2160  
TGTAATTGAA ATCTTTTAA CAAGTTCTT ATTTCCTTAC AGGGAGCTTT ACAGTAACAA 2220  
CATAACTGGC CCGATTCCTA GTAATCTTGG AAATCTGACA AACTTAGTGA GTTGGATCT 2280  
TTACTTAAAC AGCTTCCTCG GTCTTATTCC GGAATCATTG GGAAAGCTTT CAAAGCTGAG 2340  
ATTTCCTGTA GTATACATAT GCTTTACCGG CTCAGTTACA GTCTTTGTTT AATCTTAGGT 2400  
TTTGTCCAA TTTTGACTC TTGCTGAAA ATTTCACATG CAAGAATAGC CGGCTTAACA 2460  
ACAACAGTCT CACTGGGTCA ATTCTATGT CACTGACCAA TATTACTACC CTCAAGTGT 2520  
TGIGAGTCCT CTCATTAACT TTCATTATG TCTACTTCAT TCTCCCTCAG TTGATTGTT 2580  
GAGTTAACGC ACTTAAACCTT GATGGATGCA ACACAGAGAT CTATCAAATA ACAGACTCTC 2640  
TGGTCAGTT CCTGACAATG GCTCTTCCTC ACTCTTCACA CCCATCAGGT TCTATGATT 2700  
ATCCCTCTCA GTTATTTCAG TTGTTGTCAG AGTGCTGAA CTATTCTGA AACTTCATT 2760  
TCCCTGTGCA GTTTGCTAA TAACCTAGAC CTATGTGGAC CTGTTACAAG TCACCCATGT 2820  
CCTGGATCTC CCCCCGTTTC TCTCCACCA CCTTTTATTG AACCTCCOCAG AGTTTCCACC 2880  
CCGAGTAAGC CTCCCTCTT TAGTTTACAT TATAGGAAAC AGAAGATGAA ATCTTGCCT 2940  
CTCTGTCAAT CCTTTCTCTC ATATAACTCA TCTTGCAAT AAGGCAATAA CCAAATGATC 3000

TAATTTGATT TCAGGTGGGT ATGGTATAAC TGGAGCAATA GCTGGTGGAG TTGCTGCAGG 3060  
TGCTGCTTGT CTCCTTGCTG CTCCCTGCAAT AGCCTTGTCT TGGTGGCGAC GAAGAAAGCC 3120  
ACTAGATATT TTCTTCGATG TGCCCTGGTGA GTTTATTATT CGCATTTAGTT TCTGTTCTTA 3180  
GCCAGCAATT TTGTTTGCA GAAAAGTATT GGAACAACIG TTAATGAAAA TCAATACATA 3240  
AGTCATTGTT TTTTAAGTTA CAAACTCTTT TGAGTAAAAT CTGCAATTGCA AAATCTCTAT 3300  
GCAGCGGAAG AAGAICCAGA AGTTCACTTG GGACAGCTCA AGAGGTTTC TTGCGGGAG 3360  
CTACAAGTGG CGAGTGTATGG GTTTAGTAAC AAGAACATTT TGGGCAGAGG TGGGTTGGG 3420  
AAAGTCTACA AGGGACGCTT GGCAGACGGA ACTCTTGTIG CTGTCAAGAG ACTGAAGGAA 3480  
GAGCGAACTC CAGGTGGAGA GCTCCAGTTT CAAACAGAAG TAGAGATGAT AAGTATGGCA 3540  
GTTCAATCGAA ACCTGTTGAG ATTACGAGGT TTCTGTATGA CACCGACCGA GAGATTGCTT 3600  
GTGTATCCCT ACATGGCAA TGGAAAGTGT GCTTCGIGTC TCAGAGGTAA AAACAAACA 3660  
ATTAAACATC TTGTCCTCTC TCTCAATTAC TTGACGTGA AGTGTTTTT CATGTTTCC 3720  
TTTATGGGTT CATAATTGTT GGTTACACTA ATGACACAGA GAGGCCACCG TCACAACTC 3780  
CGCTTGATTG GCCAACGCGG AAGAGAATCG CGCTAGGCTC AGCTCGAGGT TTGCTTACC 3840  
TACATGATCA CTGGATCCG AAGATCACTC ACCGTGACGT AAAAGCAGCA AACATCCCT 3900  
TAGACGAAGA ATTGGAAGCG GTTGTGGAG ATTTGGGTT GGCAAAGCTA ATGGACTATA 3960  
AAGACACTCA CGTGACAACA GCAGTCCGTG GCACCATCGG TCACATCGCT CCAGAATATC 4020  
TCTCAACCGG AAAATCTCTA GAGAAAACCG ACGTTCGCG ATACGGAATC ATGCTCTAG 4080  
  
A 4081

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser Leu Ile Leu Leu  
1 5 10 15

Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu Glu Gly Asp Ala  
20 25 30

Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn Asn Val Leu Gln  
35 40 45

Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr  
50 55 60

Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu Gly Asn Ala Glu  
65 70 75 80

Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu Lys Asn Leu Gln  
85 90 95

Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro Ile Pro Ser Asn Leu Gly  
100 105 110

Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr Leu Asn Ser Phe Ser  
115 120 125

Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu Ser Lys Leu Arg Phe Leu  
130 135 140

Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser Ile Pro Met Ser Leu Thr  
145 150 155 160

Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser Asn Asn Arg Leu Ser  
165 170 175

Gly Ser Val Pro Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro Ile Ser  
180 185 190

Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro Val Thr Ser His Pro Cys  
195 200 205

Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Pro Phe Ile Gln Pro Pro  
210 215 220

Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile Thr Gly Ala Ile Ala Gly  
225 230 235 240

Gly Val Ala Ala Gly Ala Ala Leu Leu Phe Ala Ala Pro Ala Ile Ala  
245 250 255

Phe Ala Trp Trp Arg Arg Arg Lys Pro Leu Asp Ile Phe Phe Asp Val  
260 265 270

Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly Gln Leu Lys Arg Phe  
275 280 285

Ser Leu Arg Glu Leu Gln Val Ala Ser Asp Gly Phe Ser Asn Lys Asn

290	295	300	
			Ile Leu Gly Arg Gly Gly Phe Gly Lys Val Tyr Lys Gly Arg Leu Ala
305	310	315	320
			Asp Gly Thr Leu Val Ala Val Lys Arg Leu Lys Glu Glu Arg Thr Pro
	325	330	335
			Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile Ser Met Ala
	340	345	350
			Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met Thr Pro Thr
355	360	365	
			Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser Val Ala Ser
370	375	380	
			Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro Pro Leu Asp Trp Pro Thr
385	390	395	400
			Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser Tyr Leu His
405	410	415	
			Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala Ala Asn
420	425	430	
			Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp Phe Gly Leu
435	440	445	
			Ala Lys Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr Ala Val Arg
450	455	460	
			Gly Thr Ile Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly Lys Ser
465	470	475	480
			Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu Leu
	485	490	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 142..795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCGACCCACG CGTCGTCGA ACTTCAATAA AGGGGAAACC AACGTAACCC TAATTTGCT	60
TTCCTCTCTT TGTCAGAAA ATTTTCCCTT TACTCTAAA TTCCCTTTCG ATTTCCCTCT	120
CCTAAACCTC CGAAAGCTCA C ATG GCG TCT CGA AAC TAT CGG TGG GAG CTC	171
Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu	
1                  5                  10	
TTC GCA GCT TCG TTA ACC CTA ACC TTA GCT TTG ATT CAC CTG GTC GAA	219
Phe Ala Ala Ser Leu Thr Leu Thr Leu Ala Leu Ile His Leu Val Glu	
15                20                25	
GCA AAC TCC GAA GGA GAT GCT CTC TAC GCT CTT CGC CGG AGT TTG ACA	267
Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr	
30                35                40	

GAT CCA GAC CAT GTC CTC CAG AGC TGG GAT CCA ACT CTT GTT AAT CCT Asp Pro Asp His Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro	315
45 50 55	
TGT ACC TGG TTC CAT GTC ACC TGT AAC CAA GAC AAC CGC GTC ACT CGT Cys Thr Trp Phe His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg	363
60 65 70	
GIG GAT TTG GGA AAT TCA AAC CTC TCT GGA CAT CTT GCG CCT GAG CTT Val Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu	411
75 80 85 90	
GGG AAG CTT GAA CAT TTA CAG TAT CTA GAG CTC TAC AAA AAC AAC ATC Gly Lys Leu Glu His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile	459
95 100 105	
CAA GGA ACT ATA CCT TCC GAA CTT GGA AAT CTG AAG AAT CTC ATC AGC Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser	507
110 115 120	
TTG GAT CTG TAC AAC AAC AAT CTT ACA GGG ATA GTT CCC ACT TTC TTG Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Phe Leu	555
125 130 135	
GGA AAA TTG AAG TCT CTG GTC TTT TTA CGG CTT AAT GAC AAC CGA TTG Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu	603
140 145 150	
ACC GGT CCA ATC CTA GAG CAC TCA CGG CAA TCC CAA GCC TTT AAA GTT Thr Gly Pro Ile Leu Glu His Ser Arg Gln Ser Gln Ala Phe Lys Val	651
155 160 165 170	
GTT GAC GTC TCA AGC AAT GAT TTG TGT GGG ACA ATC CCA ACA AAC GGA Val Asp Val Ser Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly	699
175 180 185	
CCC TTT GCT CAC ATT CCT TTA CAG AAC TTT GAG AAC AAC CCG AGA TTG	747

Pro Phe Ala His Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu  
190 195 200

GAG GGA CCG GAA TTA CTC GGT CTT GCA AGC TAC GAC ACT AAC TGC ACC 795  
Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
205 210 215

TGAAACAACT GGCAAAACCT GAAAATGAAG AATTGGGGGG TGACCTTGTA AGAACACTTC 855  
ACCACITTTAT CAAATATCAC ATCTATTATG TAATAAGTAT ATATATGTAG TAAAAACAAA 915  
AAAAATGAAG AATCGAATCG GTAATATCAT CTGGTCTCAA TTGAGAACIT CGAGGTCTGT 975  
ATGTAAAATT TCTAAATGCG ATTTTCGCTT ACTGTAATGT TCGGTTGTGG GATTCTGAGA 1035  
AGTAACATTT GTATTGGTAT GGTATCAAGT TGTTCIGCCT TGTCTGCAA AAAAAAAA 1095  
AAAAAAAAAA A 1106

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr  
1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp  
20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu  
35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val  
50 55 60

Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser  
65 70 75 80

Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu  
85 90 95

Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser  
100 105 110

Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn  
115 120 125

Asn Leu Thr Gly Ile Val Pro Thr Phe Leu Gly Lys Leu Lys Ser Leu  
130 135 140

Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Leu Glu  
145 150 155 160

His Ser Arg Gln Ser Gln Ala Phe Lys Val Val Asp Val Ser Ser Asn  
165 170 175

Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro  
180 185 190

Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu  
195 200 205

Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
210 215

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AGTGTGAGTA ATTTAGTTTG CTTTCTCCTC TTGTGTCAGA AAATTTCCC TTTACTCTCA	60		
AATTCCCTTT CGATTTCCCT CTCTTAAACC TCCGAAAGCT CAC ATG GCG TCT CGA	115		
Met Ala Ser Arg			
1			
AAC TAT CGG TGG GAG CTC TTC GCA GCT TCG TTA ACC CTA ACC TTA GCT	163		
Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr Leu Thr Leu Ala			
5	10	15	20
TTG ATT CAC CTG GTC GAA GCA AAC TCC GAA GGA GAT GCT CTC TAC GCT	211		
Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp Ala Leu Tyr Ala			
25	30	35	
CTT CGC CGG AGT TTG ACA GAT CCA GAC CAT GTC CTC CAG AGC TGG GAT	259		
Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu Gln Ser Trp Asp			
40	45	50	

CCA ACT CTT GTT AAT CCT TGT ACC TGG TTC CAT GTC ACC TGT AAC CAA 307  
Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln  
55 60 65

GAC AAC CGC GTC ACT CGT GTG GAT TTG GGA AAT TCA AAC CTC TCT GGA 355  
Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser Asn Leu Ser Gly  
70 75 80

CAT CTT GCG CCT GAG CTT GGG AAG CTT GAA CAT TTA CAG TAT CTA GAG 403  
His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Glu  
85 90 95 100

CTC TAC AAA AAC AAC ATC CAA GGA ACT ATA CCT TCC GAA CTT GGA AAT 451  
Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn  
105 110 115

CTG AAG AAT CTC ATC AGC TTG GAT CTG TAC AAC AAC AAT CTT ACA GGG 499  
Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly  
120 125 130

ATA GTT CCC ACT TCT TTG GGA AAA TTG AAG TCT CTG GTC TTT TTA CGG 547  
Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg  
135 140 145

CTT AAT GAC AAC CGA TTG ACC GGT CCA ATC CCT AGA GCA CTC ACG GCA 595  
Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg Ala Leu Thr Ala  
150 155 160

ATC CCA AGC CTT AAA GTT GTT GAC GTC TCA AGC AAT GAT TTG TGT GGA 643  
Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn Asp Leu Cys Gly  
165 170 175 180

ACA ATC CCA ACA AAC GGA CCC TTT GCT CAC ATT CCT TTA CAG AAC TTT 691  
Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro Leu Gln Asn Phe  
185 190 195

GAG AAC AAC CCG AGA TTG GAG GGA CCG GAA TTA CTC GGT CTT GCA AGC 739

Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser  
200 205 210

TAC GAC ACT AAC TGC ACC TGAAACAACT GGCAAAACCT GAAAATGAAG 787

Tyr Asp Thr Asn Cys Thr  
215

AATTGGGGGG TGACCTTGTA AGAACACTTC ACCACTTTAT CAAATATCAC ATCTATTATG 847

TAATAAGTAT ATATATGTAG TAAAAACAAA AAAAATGAAG AATCGAATCG GTAATATCAT 907

CTGGTCTCAA TTGAGAACCTT CGAGGTCIGT AITGAAAATT TCTAAATGCG ATTTTCGCCT 967

AAATTACTCA CACT 981

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Thr  
1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp  
20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu  
35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val

50	55	60
Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser		
65	70	75
Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu		
85	90	95
Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser		
100	105	110
Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn		
115	120	125
Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu		
130	135	140
Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg		
145	150	155
160		
Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn		
165	170	175
Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro		
180	185	190
Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu		
195	200	205
Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr		
210	215	

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

T CGA CCC ACG CGT CCG CGA AAC TAT CGG TGG GAG CTC TIC GCA GCT Arg Pro Thr Arg Pro Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala	46
1 5 10 15	
TCG TTA ATC CTA ACC TTA GCT TTG ATT CAC CTG GTC GAA GCA AAC TCC Ser Leu Ile Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser	94
20 25 30	
GAA GGA GAT GCT CTT TAC GCT CTT CGC CGG AGT TTA ACA GAT CCG GAC Glu Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp	142
35 40 45	
CAT GTT CTC CAG AGC TGG GAT CCA ACT CTT GTT AAT CCT TGT ACC TGG His Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp	190
50 55 60	
TTC CAT GTC ACC TGT AAC CAA GAC AAC CGC GTC ACT CGT GTG GAT TTG Phe His Val Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu	238
65 70 75	
GGG AAT TCA AAC CTC TCT GGA CAT CTT GCG CCT GAG CTT GGG AAG CTT Gly Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu	286

80	85	90	95	
GAA CAT TTA CAG TAT CTA GAG CTC TAC AAA AAC AAC ATC CAA GGA ACT Glu His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr	100	105	110	334
ATA CCT TCC GAA CTT GGA AAT CTG AAG AAT CTC ATC AGC TTG GAT CTG Ile Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu	115	120	125	382
TAC AAC AAC AAT CTT ACA GGG ATA GTT CCC ACT TCT TTG GGA AAA TTG Tyr Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu	130	135	140	430
AAG TCT CTG GTC TTT TTA CGG CTT AAT GAC AAC CGA TTG ACG GGG CCA Lys Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro	145	150	155	478
ATC CCT AGA GCA CTC ACT GCA ATC CCA AGC CTT AAA GTT GTT GAT GTC Ile Pro Arg Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val	160	165	170	526
TCA AGC AAT GAT TTG TGT GGA ACA ATC CCA ACA AAC GGA CCT TTT GCT Ser Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala	180	185	190	574
CAC ATT CCT TTA CAG AAC TTT GAG AAC AAC CGG AGG TTG GAG GGA CCG His Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro	195	200	205	622
GAA TTA CTC GGT CTT GCA AGC TAC GAC ACT AAC TGC ACC TGAAAAAATT Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr	210	215	220	671
GGCAAAACCT GAAAATGAAG AATTGGGGGG TGACCTTGTA AGAACACTTC ACCACTTAT				731
CAAATATCAC ATCTACTATG TAATAAGTAT ATATATGTAG TCCAAAAAAA AAAAAAAA				789

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Leu Ile Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu  
20 25 30

Gly Asp Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His  
35 40 45

Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe  
50 55 60

His	Val	Thr	Cys	Asn	Gln	Asp	Asn	Arg	Val	Thr	Arg	Val	Asp	Leu	Gly						
65									70						75						80

Asn Ser Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu  
85 90 95

His Leu Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile  
100 105 110

Pro Ser Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr  
 115                    120                    125

Asn Asn Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys  
130 135 140

Ser Leu Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile  
145 150 155 160

Pro Arg Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser  
165 170 175

Ser Asn Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His  
180 185 190

Ile Pro Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu  
195 200 205

Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
210 215 220

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGA CCG ATT CAA GCC TCC GAA GGG GAC GCT CTT CAC GCG CTT CGC CGG Gly Pro Ile Gln Ala Ser Glu Gly Asp Ala Leu His Ala Leu Arg Arg	48
1 5 10 15	
AGC TTA TCA GAT CCA GAC AAT GTT GTT CAG AGT TGG GAT CCA ACT CTT Ser Leu Ser Asp Pro Asp Asn Val Val Gln Ser Trp Asp Pro Thr Leu	96
20 25 30	
GTT AAT CCT TGT ACT TGG TTT CAT GTC ACT TGT AAT CAA CAC CAT CAA Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln His His Gln	144
35 40 45	
GTC ACT CGT CTG GAT TTG GGG AAT TCA AAC TTA TCT GGA CAT CTA GTA Val Thr Arg Leu Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Val	192
50 55 60	
CCT GAA CTT GGG AAG CTT GAA CAT TTA CAA TAT CTG TAT GGA ATC ATC Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Tyr Gly Ile Ile	240
65 70 75 80	
ACT CTT TTG CCT TTT GAT TAT CTG AAA ACA TTT ACA TTA TCA GTC ACA Thr Leu Leu Pro Phe Asp Tyr Leu Lys Thr Phe Thr Leu Ser Val Thr	288
85 90 95	
CAT ATA ACA TTT TGC TTT GAG TCA TAT AGT GAA CTC TAC AAA AAC GAG His Ile Thr Phe Cys Phe Glu Ser Tyr Ser Glu Leu Tyr Lys Asn Glu	336
100 105 110	
ATT CAA GGA ACT ATA CCT TCT GAG CTT GGA AAT CTG AAG AGT CTA ATC Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Ser Leu Ile	384
115 120 125	
AGT TTG GAT CTG TAC AAC AAC AAT CTC ACC GGG AAA ATC CCA TCT TCT Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly Lys Ile Pro Ser Ser	432
130 135 140	

TTG GGA AAA TTG AAG TCA CTT GTT TTT TTG CGG CTT AAC GAA AAC CGA	480		
Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Glu Asn Arg			
145	150	155	160
TTG ACC GGT CCT ATT CCT AGA GAA CTC ACA GTT ATT TCA AGC CTT AAA	528		
Leu Thr Gly Pro Ile Pro Arg Glu Leu Thr Val Ile Ser Ser Leu Lys			
165	170	175	
GTT GTT GAT GTC TCA GGG AAT GAT TTG TGT GGA ACA ATT CCA GTA GAA	576		
Val Val Asp Val Ser Gly Asn Asp Leu Cys Gly Thr Ile Pro Val Glu			
180	185	190	
GGA CCT TTT GAA CAC ATT CCT ATG CAA AAC TTT GAG AAC AAC CTG AGA	624		
Gly Pro Phe Glu His Ile Pro Met Gln Asn Phe Glu Asn Asn Leu Arg			
195	200	205	
TTG GAG GGA CCA GAA CTA CTA GGT CTT GCG AGC TAT GAC ACC AAT TGC	672		
Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys			
210	215	220	
ACT TAAAAAGAAG TTGAAGAACC TATAAAGAAG AATGTTAGGT GACCTTGTAA	725		
Thr			
225			
GAACCTCTGTA CCAAGTGTTT GTAAATCTAT ATAGAGCCCTT GTTTCATGTT ATATATGAAA	785		
GCTTTGAGAG ACAGTAACTT GCAATGTAATT GGTATTGGTA GAAAAAGTTG AAATGAGAAT	845		
TGCTTGTAA TTGGATTTGT GTTCTTATG TAACTTGAAT TTCTTATTAA	894		

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Gly Pro Ile Gln Ala Ser Glu Gly Asp Ala Leu His Ala Leu Arg Arg  
1 5 10 15

Ser Leu Ser Asp Pro Asp Asn Val Val Gln Ser Trp Asp Pro Thr Leu  
20 25 30

Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Gln His His Gln  
35 40 45

Val Thr Arg Leu Asp Leu Gly Asn Ser Asn Leu Ser Gly His Leu Val  
50 55 60

Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu Tyr Gly Ile Ile  
65 70 75 80

Thr Leu Leu Pro Phe Asp Tyr Leu Lys Thr Phe Thr Leu Ser Val Thr  
85 90 95

His Ile Thr Phe Cys Phe Glu Ser Tyr Ser Glu Leu Tyr Lys Asn Glu  
100 105 110

Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly Asn Leu Lys Ser Leu Ile  
115 120 125

Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr Gly Lys Ile Pro Ser Ser  
130 135 140

Leu Gly Lys Leu Lys Ser Leu Val Phe Leu Arg Leu Asn Glu Asn Arg  
145 150 155 160

Leu Thr Gly Pro Ile Pro Arg Glu Leu Thr Val Ile Ser Ser Leu Lys  
165 170 175

Val Val Asp Val Ser Gly Asn Asp Leu Cys Gly Thr Ile Pro Val Glu  
180 185 190

Gly Pro Phe Glu His Ile Pro Met Gln Asn Phe Glu Asn Asn Leu Arg  
195 200 205

Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala Ser Tyr Asp Thr Asn Cys  
210 215 220

Thr  
225

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1063 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 106..759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

TOGACCCACG CGTCGGACGA AACCTTAATT TTGCTTCCTC ATCTTGTTCGAAAGATTACT 60

CAAATTCCTA TTAGATTACT CTCTCTTCGA CCTCGGATAG CTCAC ATG GCG TCT 114  
Met Ala Ser

CGA AAC TAT CGG TGG GAG CTC TTC GCA GCT TCG TTA ATC CTA ACC TTA	162
Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Ile Leu Thr Leu	
5 10 15	
GCT TTG ATT CAC CTG GTC GAA GCA AAC TCC GAA GGA GAT GCT CTT TAC	210
Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp Ala Leu Tyr	
20 25 30 35	
GCT CTT CGC CGG AGT TTA ACA GAT CCG GAC CAT GTT CTC CAG AGC TGG	258
Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu Gln Ser Trp	
40 45 50	
GAT CCA ACT CTT GTT AAT CCT TGT ACC TGG TTC CAT GTC ACC TGT AAC	306
Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn	
55 60 65	
CAA GAC AAC CGC GTC ACT CGT GTG GAT TTG GGG AAT TCA AAC CTC TCT	354
Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser Asn Leu Ser	
70 75 80	
GGA CAT CTT GCG CCT GAG CTT GGG AAG CTT GAA CAT TTA CAG TAT CTA	402
Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu Gln Tyr Leu	
85 90 95	
GAG CTC TAC AAA AAC AAC ATC CAA GGA ACT ATA CCT TCC GAA CTT GGA	450
Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser Glu Leu Gly	
100 105 110 115	
AAT CTG AAG AAT CTC ATC AGC TTG GAT CTG TAC AAC AAC AAT CTT ACA	498
Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn Asn Leu Thr	
120 125 130	
GGG ATA GTT CCC ACT TCT TTG GGA AAA TTG AAG TCT CTG GTC TTT TTA	546
Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu Val Phe Leu	
135 140 145	

CGG CTT AAT GAC AAC CGA TTG ACG GGG CCA ATC CCT AGA GCA CTC ACT	594		
Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg Ala Leu Thr			
150	155	160	
GCA ATC CCA AGC CTT AAA GTT GTT GAT GTC TCA AGC AAT GAT TTG TGT	642		
Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn Asp Leu Cys			
165	170	175	
GGA ACA ATC CCA ACA AAC GGA CCT TTT GCT CAC ATT CCT TTA CAG AAC	690		
Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro Leu Gln Asn			
180	185	190	195
TTT GAG AAC AAC CCG AGG TTG GAG GGA CCG GAA TTA CTC GGT CTT GCA	738		
Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu Gly Leu Ala			
200	205	210	
AGC TAC GAC ACT AAC TGC ACC TGAAAAAATT GGCAAAACCT GAAAATGAAG	789		
Ser Tyr Asp Thr Asn Cys Thr			
215			
AATTGGGGGG TGACCTTGTA AGAACACTTC ACCACTTTAT CAAATATCAC ATCTACTATG	849		
TAATAAGTAT ATATATGTAG TCCAAAAAAA AAATGAAGAA TCGAATCAGT AATATCATCT	909		
GGCTCTCAATT GAGAACCTTG AGGCTCTGIGT ATGTAAAATT TCTAAATGCG ACTTTCGCGT	969		
ACTGTAAATGT TCGGTGTGG GATTCTGAGA AGTAACATTT GTATTGGTAT GGTATCAAGT	1029		
TGTTCTGCCT TGTCTGCAA AAAA AAAAAA AAAAA	1063		

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Ala Ser Arg Asn Tyr Arg Trp Glu Leu Phe Ala Ala Ser Leu Ile  
1 5 10 15

Leu Thr Leu Ala Leu Ile His Leu Val Glu Ala Asn Ser Glu Gly Asp  
20 25 30

Ala Leu Tyr Ala Leu Arg Arg Ser Leu Thr Asp Pro Asp His Val Leu  
35 40 45

Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val  
50 55 60

Thr Cys Asn Gln Asp Asn Arg Val Thr Arg Val Asp Leu Gly Asn Ser  
65 70 75 80

Asn Leu Ser Gly His Leu Ala Pro Glu Leu Gly Lys Leu Glu His Leu  
85 90 95

Gln Tyr Leu Glu Leu Tyr Lys Asn Asn Ile Gln Gly Thr Ile Pro Ser  
100 105 110

Glu Leu Gly Asn Leu Lys Asn Leu Ile Ser Leu Asp Leu Tyr Asn Asn  
115 120 125

Asn Leu Thr Gly Ile Val Pro Thr Ser Leu Gly Lys Leu Lys Ser Leu  
130 135 140

Val Phe Leu Arg Leu Asn Asp Asn Arg Leu Thr Gly Pro Ile Pro Arg  
145 150 155 160

Ala Leu Thr Ala Ile Pro Ser Leu Lys Val Val Asp Val Ser Ser Asn

165

170

175

Asp Leu Cys Gly Thr Ile Pro Thr Asn Gly Pro Phe Ala His Ile Pro  
180 185 190

Leu Gln Asn Phe Glu Asn Asn Pro Arg Leu Glu Gly Pro Glu Leu Leu  
195 200 205

Gly Leu Ala Ser Tyr Asp Thr Asn Cys Thr  
210 215

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

- (B) CLONE: SERK gene cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 195..2069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGATTTTAT TTTATTTTACTCTTTGTT TGTTTTAATG CTAATGGGTT TTTAAAAGGG	60
TTATCGAAAA AATGAGTGAG TTGTTGTTGA GGTGTCCTCT GTAAAGTGTG AATGGTGGTG	120
ATTTTCGGAA GTTACGGTTT TCTCGGATCT GAAGAGATCA AATCAAGATT CGAAATTAC	180
CATTGTTGTTGTT TGAA ATG GAG TCG AGT TAT GTG GTG TTT ATC TTA CTT TCA Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser	230
1 5 10	
CTG ATC TTA CTT CCG AAT CAT TCA CTG TGG CTT GCT TCT GCT AAT TTG Leu Ile Leu Leu Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu	278
15 20 25	
GAA GGT GAT GCT TTG CAT ACT TTG AGG GTT ACT CTA GTT GAT CCA AAC Glu Gly Asp Ala Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn	326
30 35 40	
AAT GTC TTG CAG AGC TGG GAT CCT ACG CTA GTG AAT CCT TGC ACA TGG Asn Val Leu Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp	374
45 50 55 60	
TTC CAT GTC ACT TGC AAC AAC GAG AAC AGT GTC ATA AGA GTT GAT TTG Phe His Val Thr Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu	422
65 70 75	
GGG AAT GCA GAG TTA TCT GGC CAT TTA GTT CCA GAG CTT GGT GTG CTC Gly Asn Ala Glu Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu	470
80 85 90	
AAG AAT TTG CAG TAT TTG GAG CTT TAC AGT AAC AAC ATA ACT GGC CCG Lys Asn Leu Gln Tyr Leu Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro	518
95 100 105	
ATT CCT AGT AAT CTT GGA AAT CTG ACA AAC TTA GTG AGT TTG GAT CTT	566

Ile Pro Ser Asn Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu  
110 115 120

TAC TTA AAC AGC TTC TCC GGT CCT ATT CCG GAA TCA TTG GGA AAG CTT 614  
Tyr Leu Asn Ser Phe Ser Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu  
125 130 135 140

TCA AAG CTG AGA TTT CTC CGG CTT AAC AAC AAC AGT CTC ACT GGG TCA 662  
Ser Lys Leu Arg Phe Leu Arg Leu Asn Asn Asn Ser Leu Thr Gly Ser  
145 150 155

ATT CCT ATG TCA CTG ACC AAT ATT ACT ACC CTT CAA GTG TTA GAT CTA 710  
Ile Pro Met Ser Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu  
160 165 170

TCA AAT AAC AGA CTC TCT GGT TCA GTT CCT GAC AAT GGC TCC TIC TCA 758  
Ser Asn Asn Arg Leu Ser Gly Ser Val Pro Asp Asn Gly Ser Phe Ser  
175 180 185

CTC TTC ACA CCC ATC AGT TTT GCT AAT AAC TTA GAC CTA TGT GGA CCT 806  
Leu Phe Thr Pro Ile Ser Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro  
190 195 200

GTT ACA AGT CAC CCA TGT CCT GGA TCT CCC CGG TTT TCT CCT CCA CCA 854  
Val Thr Ser His Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro  
205 210 215 220

CCT TTT ATT CAA CCT CCC CCA GTT TCC ACC CGG AGT GGG TAT GGT ATA 902  
Pro Phe Ile Gln Pro Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile  
225 230 235

ACT GGA GCA ATA GCT GGT GGA GTT GCT GCA GGT GCT GCT TTG CCC TTT 950  
Thr Gly Ala Ile Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Pro Phe  
240 245 250

GCT GCT CCT GCA ATA GCC TTT GCT TGG TGG CGA CGA AGA AGC CCA CTA 998  
Ala Ala Pro Ala Ile Ala Phe Ala Trp Trp Arg Arg Arg Ser Pro Leu

255	260	265	
GAT ATT TTC TTC GAT GTC CCT GCC GAA GAA GAT CCA GAA GTT CAT CTG			1046
Asp Ile Phe Phe Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu			
270	275	280	
GGA CAG CTC AAG AGG TTT TCT TTG CGG GAG CTA CAA GTG GCG AGT GAT			1094
Gly Gln Leu Lys Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Ser Asp			
285	290	295	300
GGG TTT AGT AAC AAG AAC ATT TTG GGC AGA GGT GGG TTT GGG AAA GTC			1142
Gly Phe Ser Asn Lys Asn Ile Leu Gly Arg Gly Gly Phe Gly Lys Val			
305	310	315	
TAC AAG GGA CGC TTG GCA GAC GGA ACT CTT GTT GCT GTC AAG AGA CTG			1190
Tyr Lys Gly Arg Leu Ala Asp Gly Thr Leu Val Ala Val Lys Arg Leu			
320	325	330	
AAG GAA GAG CGA ACT CCA GGT GGA GAG CTC CAG TTT CAA ACA GAA GTA			1238
Lys Glu Glu Arg Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val			
335	340	345	
GAG ATG ATA AGT ATG GCA GTT CAT CGA AAC CTG TTG AGA TTA CGA GGT			1286
Glu Met Ile Ser Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly			
350	355	360	
TTC TGT ATG ACA CCG ACC GAG AGA TTG CTT GTG TAT CCT TAC ATG GCC			1334
Phe Cys Met Thr Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala			
365	370	375	380
AAT GGA AGT GTT GCT TCG TGT CTC AGA GAG AGG CCA CCG TCA CAA CCT			1382
Asn Gly Ser Val Ala Ser Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro			
385	390	395	
CCG CTT GAT TGG CCA ACG CGG AAG AGA ATC GCG CTA GGC TCA GCT CGA			1430
Pro Leu Asp Trp Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg			
400	405	410	

GGT TTG TCT TAC CTA CAT GAT CAC TGC GAT CCG AAG ATC ATT CAC CGT	1478	
Gly Leu Ser Tyr Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg		
415	420	425
GAC GTA AAA GCA GCA AAC ATC CTC TTA GAC GAA GAA TTC GAA GCG GTT	1526	
Asp Val Lys Ala Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val		
430	435	440
GTT GGA GAT TTC GGG TTG GCA AAG CTT ATG GAC TAT AAA GAC ACT CAC	1574	
Val Gly Asp Phe Gly Leu Ala Lys Leu Met Asp Tyr Lys Asp Thr His		
445	450	455
460		
GTG ACA ACA GCA GTC CGT GGC ACC ATC GGT CAC ATC GCT CCA GAA TAT	1622	
Val Thr Thr Ala Val Arg Gly Thr Ile Gly His Ile Ala Pro Glu Tyr		
465	470	475
CTC TCA ACC GGA AAA TCT TCA GAG AAA ACC GAC GTT TTC GGA TAC GGA	1670	
Leu Ser Thr Gly Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly		
480	485	490
ATC ATG CTT CTA GAA CTA ATC ACA GGA CAA AGA GCT TTC GAT CTC GCT	1718	
Ile Met Leu Leu Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala		
495	500	505
CGG CTA GCT AAC GAC GAC GTC ATG TTA CTT GAC TGG GTG AAA GGA	1766	
Arg Leu Ala Asn Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Gly		
510	515	520
TTG TTG AAG GAG AAG AAG CTA GAG ATG TTA GTG GAT CCA GAT CTT CAA	1814	
Leu Leu Lys Glu Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Gln		
525	530	535
540		
ACA AAC TAC GAG GAG AGA GAA CTG GAA CAA GTG ATA CAA GTG GCG TTG	1862	
Thr Asn Tyr Glu Glu Arg Glu Leu Glu Gln Val Ile Gln Val Ala Leu		
545	550	555

CTA TGC ACG CAA GGA TCA CCA ATG GAA AGA CCA AAG ATG TCT GAA GTT Leu Cys Thr Gln Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val	560	565	570	1910
GTA AGG ATG CTG GAA GGA GAT GGG CTT GCG GAG AAA TGG GAC GAA TGG Val Arg Met Leu Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp	575	580	585	1958
CAA AAA GTT GAG ATT TTG AGG GAA GAG ATT GAT TTG AGT CCT AAT CCT Gln Lys Val Glu Ile Leu Arg Glu Glu Ile Asp Leu Ser Pro Asn Pro	590	595	600	2006
AAC TCT GAT TGG ATT CTT GAT TCT ACT TAC AAT TTG CAC GCC GTT GAG Asn Ser Asp Trp Ile Leu Asp Ser Thr Tyr Asn Leu His Ala Val Glu	605	610	615	2054
TTA TCT GGT CCA AGG TAAAAAAAAA AAAAAAAA Leu Ser Gly Pro Arg	625			2089

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Glu Ser Ser Tyr Val Val Phe Ile Leu Leu Ser Leu Ile Leu Leu	1	5	10	15
Pro Asn His Ser Leu Trp Leu Ala Ser Ala Asn Leu Glu Gly Asp Ala	20	25	30	

Leu His Thr Leu Arg Val Thr Leu Val Asp Pro Asn Asn Val Leu Gln

35

40

45

Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr

50

55

60

Cys Asn Asn Glu Asn Ser Val Ile Arg Val Asp Leu Gly Asn Ala Glu

65

70

75

80

Leu Ser Gly His Leu Val Pro Glu Leu Gly Val Leu Lys Asn Leu Gln

85

90

95

Tyr Leu Glu Leu Tyr Ser Asn Asn Ile Thr Gly Pro Ile Pro Ser Asn

100

105

110

Leu Gly Asn Leu Thr Asn Leu Val Ser Leu Asp Leu Tyr Leu Asn Ser

115

120

125

Phe Ser Gly Pro Ile Pro Glu Ser Leu Gly Lys Leu Ser Lys Leu Arg

130

135

140

Phe Leu Arg Leu Asn Asn Ser Leu Thr Gly Ser Ile Pro Met Ser

145

150

155

160

Leu Thr Asn Ile Thr Thr Leu Gln Val Leu Asp Leu Ser Asn Asn Arg

165

170

175

Leu Ser Gly Ser Val Pro Asp Asn Gly Ser Phe Ser Leu Phe Thr Pro

180

185

190

Ile Ser Phe Ala Asn Asn Leu Asp Leu Cys Gly Pro Val Thr Ser His

195

200

205

Pro Cys Pro Gly Ser Pro Pro Phe Ser Pro Pro Pro Pro Phe Ile Gln

210

215

220

Pro Pro Pro Val Ser Thr Pro Ser Gly Tyr Gly Ile Thr Gly Ala Ile  
225 230 235 240

Ala Gly Gly Val Ala Ala Gly Ala Ala Leu Pro Phe Ala Ala Pro Ala  
245 250 255

Ile Ala Phe Ala Trp Trp Arg Arg Arg Ser Pro Leu Asp Ile Phe Phe  
260 265 270

Asp Val Pro Ala Glu Glu Asp Pro Glu Val His Leu Gly Gln Leu Lys  
275 280 285

Arg Phe Ser Leu Arg Glu Leu Gln Val Ala Ser Asp Gly Phe Ser Asn  
290 295 300

Lys Asn Ile Leu Gly Arg Gly Phe Gly Lys Val Tyr Lys Gly Arg  
305 310 315 320

Leu Ala Asp Gly Thr Leu Val Ala Val Lys Arg Leu Lys Glu Glu Arg  
325 330 335

Thr Pro Gly Gly Glu Leu Gln Phe Gln Thr Glu Val Glu Met Ile Ser  
340 345 350

Met Ala Val His Arg Asn Leu Leu Arg Leu Arg Gly Phe Cys Met Thr  
355 360 365

Pro Thr Glu Arg Leu Leu Val Tyr Pro Tyr Met Ala Asn Gly Ser Val  
370 375 380

Ala Ser Cys Leu Arg Glu Arg Pro Pro Ser Gln Pro Pro Leu Asp Trp  
385 390 395 400

Pro Thr Arg Lys Arg Ile Ala Leu Gly Ser Ala Arg Gly Leu Ser Tyr  
405 410 415

Leu His Asp His Cys Asp Pro Lys Ile Ile His Arg Asp Val Lys Ala

420

425

430

Ala Asn Ile Leu Leu Asp Glu Glu Phe Glu Ala Val Val Gly Asp Phe  
435 440 445

Gly Leu Ala Lys Leu Met Asp Tyr Lys Asp Thr His Val Thr Thr Ala  
450 455 460

Val Arg Gly Thr Ile Gly His Ile Ala Pro Glu Tyr Leu Ser Thr Gly  
465 470 475 480

Lys Ser Ser Glu Lys Thr Asp Val Phe Gly Tyr Gly Ile Met Leu Leu  
485 490 495

Glu Leu Ile Thr Gly Gln Arg Ala Phe Asp Leu Ala Arg Leu Ala Asn  
500 505 510

Asp Asp Asp Val Met Leu Leu Asp Trp Val Lys Gly Leu Leu Lys Glu  
515 520 525

Lys Lys Leu Glu Met Leu Val Asp Pro Asp Leu Gln Thr Asn Tyr Glu  
530 535 540

Glu Arg Glu Leu Glu Gln Val Ile Gln Val Ala Leu Leu Cys Thr Gln  
545 550 555 560

Gly Ser Pro Met Glu Arg Pro Lys Met Ser Glu Val Val Arg Met Leu  
565 570 575

Glu Gly Asp Gly Leu Ala Glu Lys Trp Asp Glu Trp Gln Lys Val Glu  
580 585 590

Ile Leu Arg Glu Glu Ile Asp Leu Ser Pro Asn Pro Asn Ser Asp Trp  
595 600 605

Ile Leu Asp Ser Thr Tyr Asn Leu His Ala Val Glu Leu Ser Gly Pro  
610 615 620

Arg

625

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What is Claimed is:

1. A method of producing apomictic seeds comprising the steps of:
  - (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic,
  - (ii) regenerating the thus transformed material into plants, or carpel-containing parts thereof, and
  - (iii) expressing the sequence in the vicinity of the embryo sac.
2. A method according to the preceding claim, wherein the apomictic seeds are of the adventitious embryony type.
3. A method according to either of the preceding claims, wherein expression of the sequence yields a protein kinase capable of spanning a plant cell membrane.
4. A method according to the preceding claim wherein the kinase is capable of autophosphorylation.
5. A method according to any of the preceding claims, wherein the protein is a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain.
6. A method according to the preceding claim, wherein the protein lacks a functional ligand binding domain but comprises a proline box, a transmembrane domain, a kinase domain and a protein binding domain.
7. A method according to any preceding claim, wherein once incorporated into the cell membrane, the protein binding domain is located intra-cellularly.
8. A method according to any preceding claim, wherein the sequence further encodes a cell membrane targeting sequence.

9. A method according to any preceding claim, wherein the sequence is that depicted in SEQ ID Nos. 1 or 2 or is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
10. A method according to any preceding claim, wherein the sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the sequence is to be inserted are used so that expression of the thus modified sequence in the said plant yields substantially similar protein to that obtained by expression of the unmodified sequence in the organism in which the protein is endogenous.
11. A method according to any preceding claim, wherein expression of the sequence is under control of an inducible or developmentally regulated promoter.
12. A method according to the preceding claim, wherein expression of the sequence is under control of one of the following: a promoter which regulates expression of SERK genes *in planta*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*.
13. A method according to any of the preceding claims, wherein the sequence is expressed in the somatic cells of the embryo sac, ovary wall, nucellus, or integuments.
14. A method according to any of the preceding claims, wherein the endosperm within the apomictic seed results from fusion of polar nuclei within the embryo sac with a pollen-derived male gamete nucleus.
15. A method according to the preceding claim, wherein the sequence encoding the protein is expressed prior to fusion of the polar nuclei with the male gamete nucleus.

16. DNA comprising a sequence encoding a protein the presence of which in an active form in a cell, or membrane thereof, renders said cell embryogenic.
17. DNA according to claim 16, wherein the protein is a leucine rich repeat receptor like kinase and comprises a ligand binding domain, a proline box, a transmembrane domain, a kinase domain and a protein binding domain, the ligand binding domain optionally being absent or functionally inactive.
18. DNA according to either of claims 16 or 17 comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn.
19. DNA according to claim 18 comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn  
with Xaa being a variable amino acid, but preferably Leu or Val.
20. DNA according to claim 19 comprising a DNA sequence encoding a N-terminal protein fragment having the following amino acid sequence: Val Xaa Gln Ser Trp Asp Pro Thr Leu Val Asn Pro Cys Thr Trp Phe His Val Thr Cys Asn Xab Xac Xad Xae Val Xaf Arg Val Asp Leu Gly Asn Xag Xah Leu Ser Gly His Leu Xai Pro Glu Leu Gly Xaj Leu Xak Xal Leu Gln  
with Xaa to Xak being a variable amino acid, but preferably  
  
Xaa = Leu or Val  
  
Xab = Asn or Gln  
  
Xac = Glu or Asp or His  
  
Xad = Asn or His  
  
Xae = Ser or Arg or Gln  
  
Xaf = Ile or Thr  
  
Xag = Ala or Ser  
  
Xah = Glu or Asn  
  
Xai = Val or Ala  
  
Xaj = Val or Lys  
  
Xak = Lys or Glu

Xai=Asn or His

21. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID No. 3, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
22. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID No. 21, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
23. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID No. 33, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
24. DNA comprising a sequence encoding a protein having the sequence depicted in SEQ ID Nos. 23, 25, 27, 29 and 31, or a protein substantially similar thereto which is capable of being membrane bound and which has kinase activity.
25. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID Nos. 1 or 2 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
26. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID No: 20 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.
27. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID No: 32 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.

28. DNA according to any preceding claim, comprising a DNA having the sequence depicted in SEQ ID Nos: 22, 24, 26, 28 and 30 or a sequence which is complementary to one which hybridizes under stringent conditions with the said sequences and which encodes a membrane bound protein having kinase activity.

29. DNA according to any of the preceding claims, which further encodes a cell membrane targeting sequence.

30. DNA according to any one of the preceding claims, in which the protein encoding region is under expression control of a developmentally regulated or inducible promoter.

31. DNA according to claim 30, wherein the promoter is one of the following: a promoter which regulates expression of SERK genes *in planta*, the carrot chitinase DcEP3-1 gene promoter, the *Arabidopsis* AtChitIV gene promoter, the *Arabidopsis* LTP-1 gene promoter, the *Arabidopsis* bel-1 gene promoter, the petunia fbp-7 gene promoter, the *Arabidopsis* ANT gene promoter, the promoter of the O126 gene from *Phalaenopsis*; the *Arabidopsis* DMC1 promoter, the pTA7001 inducible promoter.

32. DNA according to any preceding claim, wherein said DNA is a recombinant DNA.

33. DNA according to any preceding claim, wherein the sequence is modified in that known mRNA instability motifs or polyadenylation signals are removed and/or codons which are preferred by the plant into which the DNA is to be inserted are used so that expression of the thus modified DNA in the said plant yields substantially similar protein to that obtained by expression of the unmodified DNA in the organism in which the protein is endogenous.

34. DNA which is complementary to that which hybridizes under stringent conditions with the DNA of any one of claims 16 to 29.

35. A vector containing a DNA sequence as claimed in any one of claims 16 to 34.

36. Plant cell transformed with the DNA of any one of claims 16 to 34 or the vector of claim 35, which contains the DNA stably incorporated into its genome.

37. Plant cell according to claim 36, which is part of a whole plant.
38. Plants transformed with the DNA of any one of claims 16 to 34 or the vector of claim 35, the progeny of such plants which contain the DNA stably incorporated, and/or the apomictic seeds of such plants or such progeny.
39. Plants transformed with the DNA comprised by the recombinant DNA of claims 16 to 34.
40. Use of the DNA of any one of claims 16-34 in the manufacture of apomictic seeds.
41. Plants which are derived from apomictic seeds obtainable by the method of any one of claims 1-15 or 40.
42. A method of obtaining cultivars comprising the steps of fertilizing plants with the pollen of the plants of either of claims 38, 39 or 40 and cultivars which result from the said method.
43. A method of obtaining embryogenic cells in plant material, comprising transforming the material with a recombinant DNA sequence as claimed in any one of claims 16-34, the DNA comprised by the recombinant DNA of any one of claims 16 to 34, or the vector of claim 35, expressing the sequence in the material or derivatives thereof and subjecting the said material or derivatives to a compound which acts as a ligand for the gene product of the said sequence.
44. A method according to the preceding claim, wherein the sequence encodes a leucine rich repeat receptor like kinase, and the compound is a phyto-hormone.
45. A method of generating somatic embryos under *in vitro* conditions wherein the SERK protein is overexpressed ectopically.
46. A bag containing apomictic seeds obtainable by the method of any one of claims 1-15 or 40.

ABSTRACT

The present invention provides, *inter alia*, a method of producing apomictic seeds comprising the steps of:

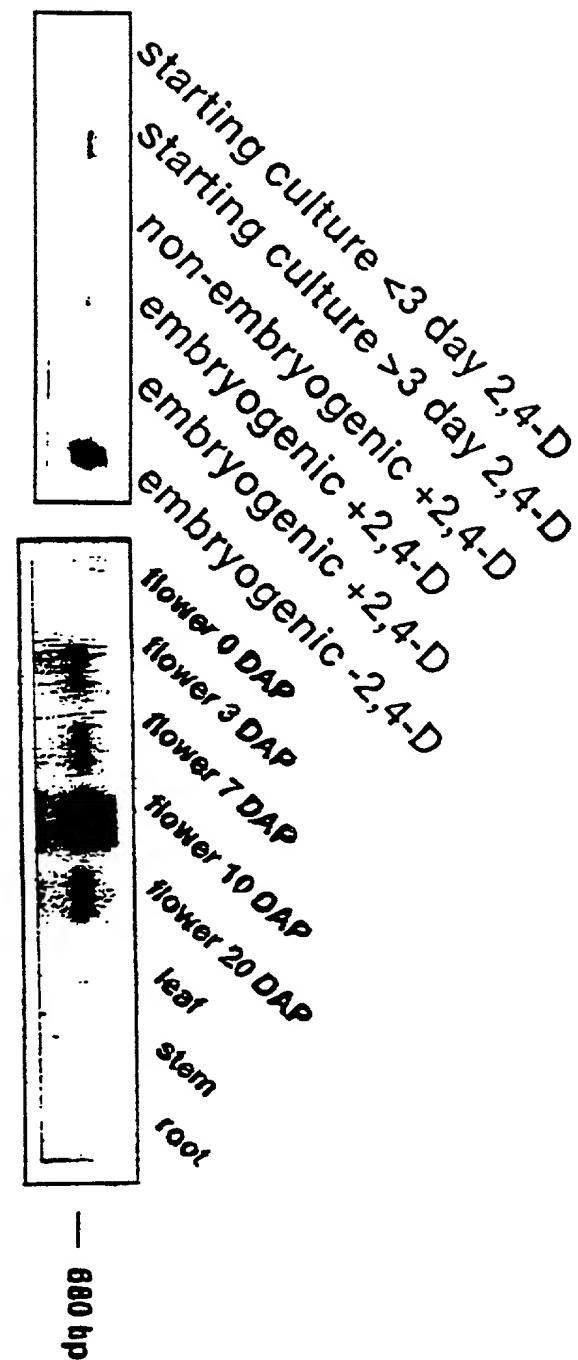
- (i) transforming plant material with a nucleotide sequence encoding a protein the presence of which in a cell, or membrane thereof, renders said cell embryogenic,
- (ii) regenerating the thus transformed material into plants, or carpel containing parts thereof, and
- (iii) expressing the sequence in the vicinity of the embryo sac.

The protein may be a leucine repeat rich receptor kinase which preferably is modified to the extent that the ligand binding domain is deleted or functionally inactivated.

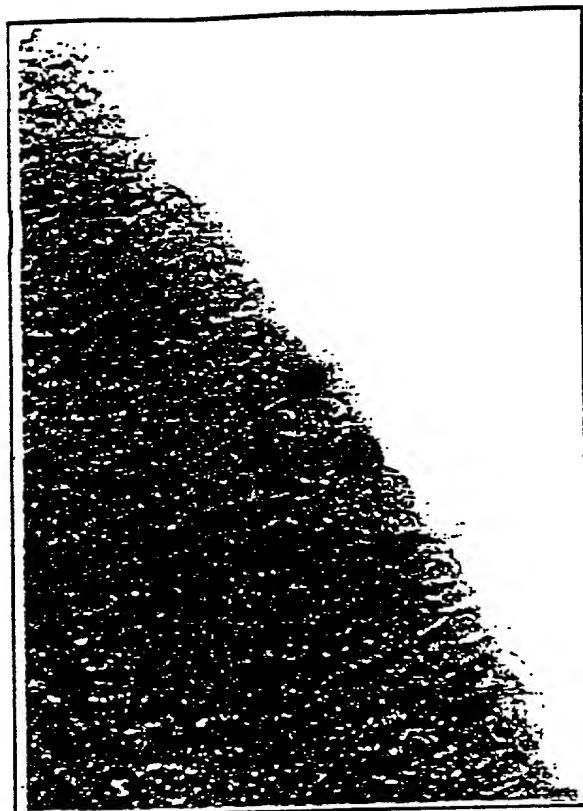
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Figure 1



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A



B

Figure 2

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Figure 3

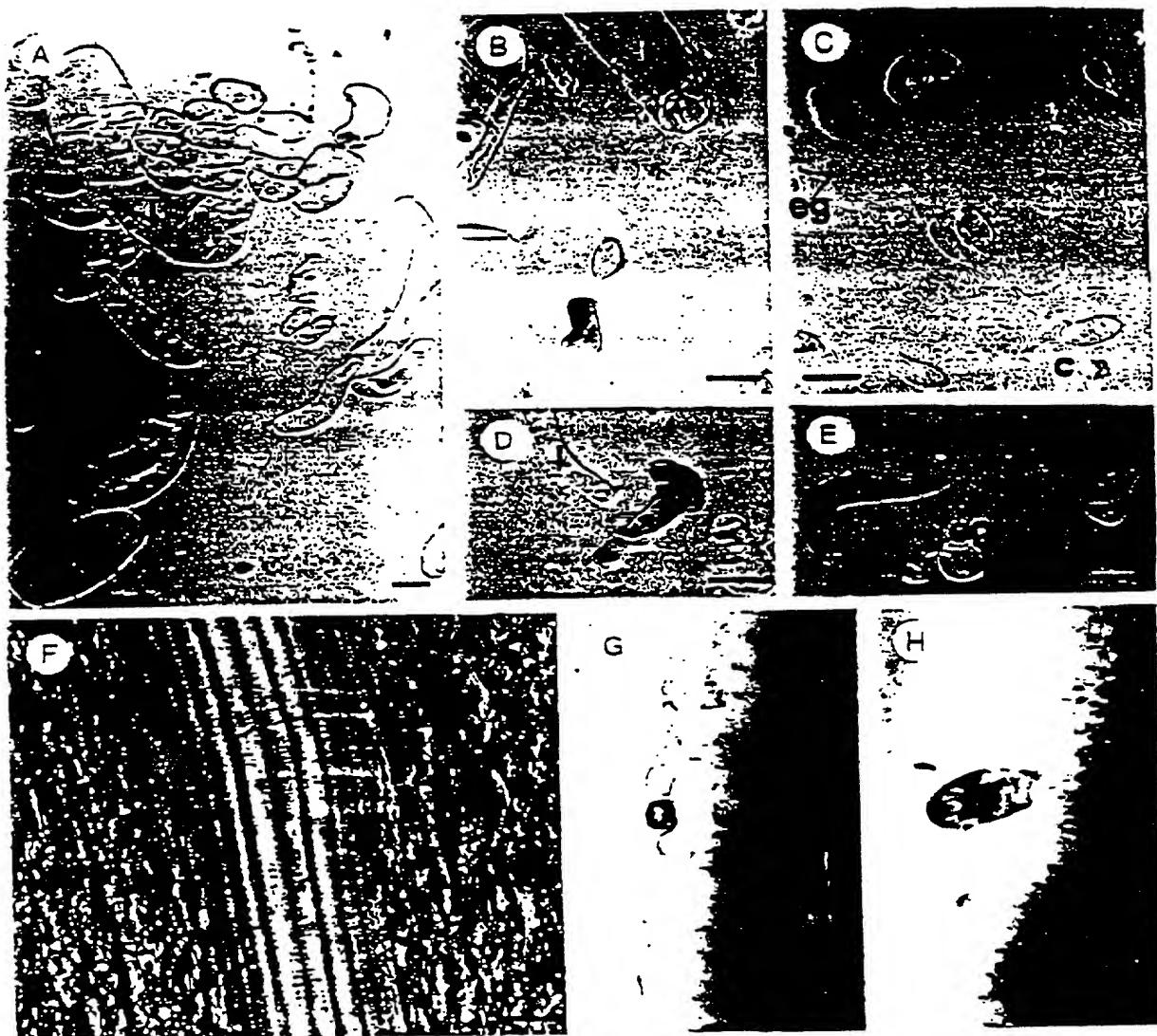


Fig  
6

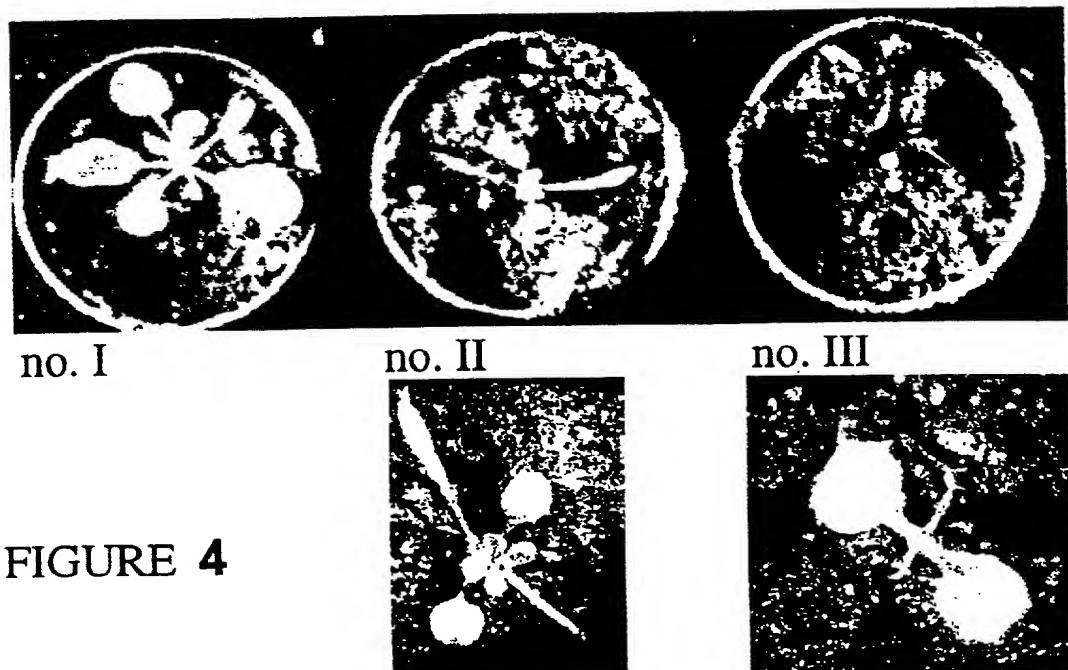
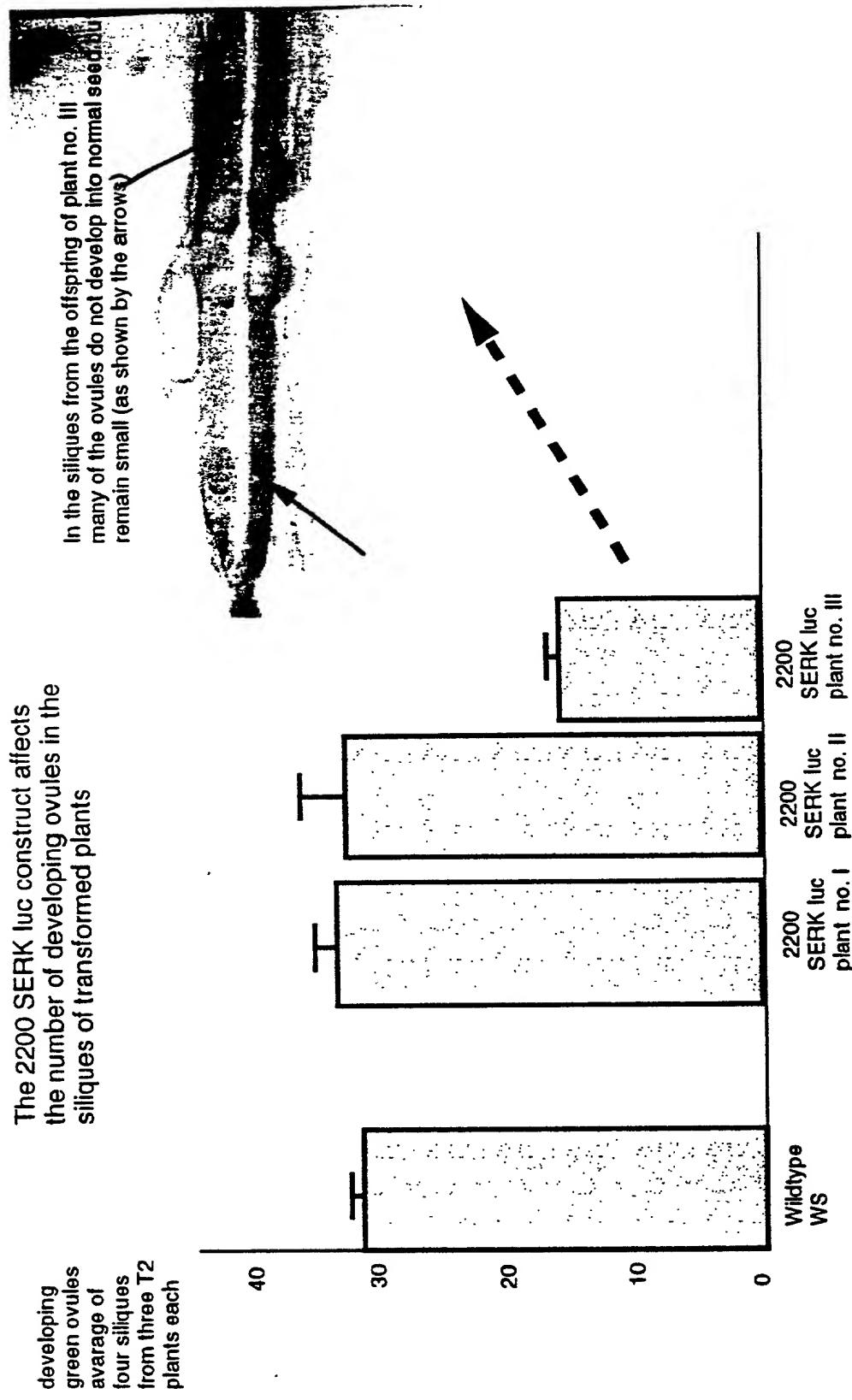


FIGURE 4

Arabidopsis WS plants transformed with the 2200 bp SERK-luciferase construct show a phenotype at the seedling level. Pictures were taken at 28 days after germination of T2 seeds. In plant II and III no clear shoot meristem is visible at the seedlings stage, 7 days after germination. The first two leaves, if they develop at all, are needle-shaped as shown on the pictures taken at 28 days after germination. At this time plant I, which shows no clear phenotype, already starts flowering. Secondary shoot meristems are already developing in plant no. II and will also develop later from no. III. Shoot meristems, inflorescences and normal flowers eventually develop on all plants.

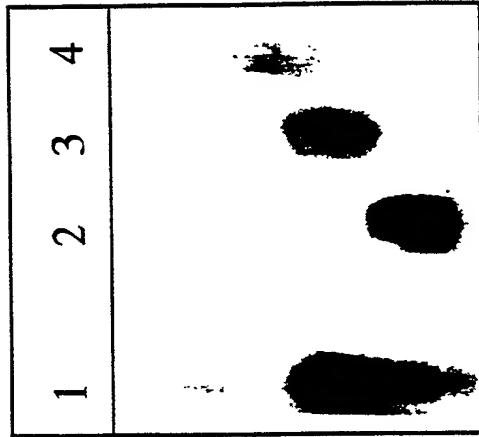
**Figure 5**

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## Figure 6

Purified SERK fusion protein is used for autophosphorylation in vitro. Most, if not all of the phosphorylation of SERK takes place on threonine residues.

lane 1, the purified SERK fusion protein; lane 2, serine phosphate; lane 3, threonine phosphate; lane 4, tyrosine phosphate.



**DECLARATION AND POWER OF ATTORNEY FOR UNITED STATES PATENT APPLICATION**

Original

Supplemental

Substitute

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a United States patent is sought on the invention entitled

**PRODUCTION OF APOMICTIC SEED**

the specification of which:

is attached hereto.

was filed on \_\_\_\_\_ as Application No. \_\_\_\_\_  
(day/month/year)

and, if this box () contains an **x**

was amended on \_\_\_\_\_  
(day/month/year)

was filed as Patent Cooperation Treaty international Application No.

PCT/EP 97/02443 on 13/05/1997  
(day/month/year)

and, if this box () contains an **x**

entered the national stage in the United States and was accorded Application No.

\_\_\_\_\_ and, if this box () contains an **x**

was amended, subsequent to entry into the national stage, on \_\_\_\_\_  
(day/month/year)

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment(s) referred to above and, if this application was filed as a Patent Cooperation Treaty international application, by any amendments made during the international stage (including any made under Patent Cooperation Treaty Rule 91, Article 19 and Article 34).

I acknowledge my duty to disclose all information which is known by me to be material to the patentability of this application as defined in 37 C.F.R. § 1.56.

I hereby claim the benefit under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate listed below and under 35 U.S.C. §365(a) of any Patent Cooperation Treaty international application(s) designating at least one country other than the United States listed below and have also listed below any foreign application(s) for patent or inventor's certificate and Patent Cooperation Treaty international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application the priority of which is claimed for that subject matter:

COUNTRY/REGION (OR P.C.T.)	APPLICATION No.	FILING DATE (day/month/year)	PRIORITY CLAIMED	
Great Britain	9610044.1	14/05/96	<input checked="" type="checkbox"/> Yes	<input type="checkbox"/> No
			<input type="checkbox"/> Yes	<input type="checkbox"/> No
			<input type="checkbox"/> Yes	<input type="checkbox"/> No
			<input type="checkbox"/> Yes	<input type="checkbox"/> No
			<input type="checkbox"/> Yes	<input type="checkbox"/> No

I hereby claim the benefit under 35 U.S.C. § 119 (e) of any United States provisional application(s) listed below:

APPLICATION NO.	FILING DATE (day/month/year)

I hereby claim the benefit under 35 U.S.C. §120 of any United States application(s) listed below and under 35 U.S.C. §365(c) of any Patent Cooperation Treaty international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of 35 U.S.C. §112, I acknowledge my duty to disclose all information known to me to be material to patentability as defined in 37 C.F.R. §1.56 which became available between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

United States Application No.	United States Filing Date (day/month/year)	Status (Pending, Abandoned or U.S. Patent No.)	International Application No. and Filing Date

I hereby appoint the registered practitioners associated with Customer No. 001095, respectively and individually, as my attorneys and agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith.

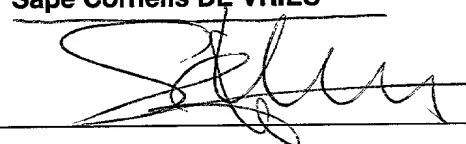
If these brackets contain an X [X], I hereby authorize the registered practitioners associated with Customer No. 001095 and any others acting on my behalf to take any action relating to this application based on communications from the Patents and Trademarks Division of Novartis Services AG, Basle, Switzerland, or an affiliate thereof or a successor thereto, without direct communication from me.

Please address all communications to Michael W. Glynn, Novartis Corporation, Patent and Trademark Department, 564 Morris Avenue, Summit, NJ 07901-1027.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. §1001 and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Full name of sole  
or first joint inventor

**Sape Cornelis DE VRIES**



Date

12 10 1998  
(day/month/year)

Inventor's signature

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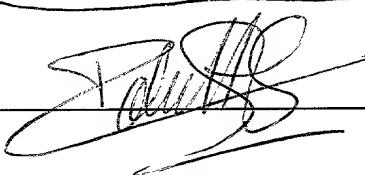
**Roghorst 192, 6708 KS Wageningen  
Netherlands**

**IMPORTANT:** Before this declaration is signed, the patent application (the specification, the claims and this declaration) must be read and understood by each person signing it, and no changes may be made in the application after this declaration has been signed.

Full name of second joint inventor, if any

**Valérie France Gabrielle HECHT**

Inventor's signature



Date

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(day/month/year)

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Citizenship

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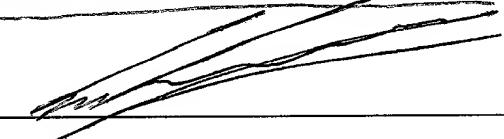
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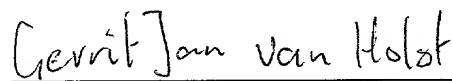
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**Gerrit Jan VAN HOLST**

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Date

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